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OM protein - protein search, using sw model
Run On: September 13, 2000, 02:22:07 ; Search time 17.65 Seconds
(without alignments)
18.788 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 14
Sequence: 1 AEFHRWSSYVHWK 14
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 188963 seqs, 23686106 residues
Word size : 0
Total number of hits satisfying chosen parameters: 188963
Minimum DB seq length: 0
Maximum DB seq length: 100000
Post-processing: Listing first 45 summaries
Database : A_Genseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	1 W35340	Human acetylcholin
2	14	100.0	39	1 R77010	Alternative human
3	14	100.0	45	1 W48800	C-terminal fragmen
4	14	100.0	45	1 W68144	Human AChE splice
5	14	100.0	45	1 W74586	Amino acid sequenc
6	14	100.0	500	1 R06990	Human foetal acety
7	14	100.0	613	1 R06989	Human acetylcholin
8	14	100.0	614	1 R80726	Human acetylcholin
9	9	64.3	575	1 W39078	Torpedo californic
10	9	64.3	575	1 W39079	Torpedo californic
11	5	35.7	12	1 R63398	Peptide fragment o
12	5	35.7	111	1 W61227	Streptococcus pneu
13	5	35.7	136	1 W74955	Human secreted pro
14	5	35.7	256	1 P70559	Product of ORF 1 f
15	5	35.7	261	1 R63805	Polyhydroxyalkanoa
16	5	35.7	319	1 R63349	Hepatitis C virus
17	4	28.6	4	1 W35341	Human acetylcholin
18	4	28.6	4	1 W35342	Human acetylcholin
19	4	28.6	4	1 W35343	Human acetylcholin
20	4	28.6	8	1 R25957	ICAM-1 inhibiting
21	4	28.6	10	1 W32750	Human platelet gly
22	4	28.6	10	1 W76015	LM609 grafted anti
23	4	28.6	12	1 R78593	LACI K1 derivative
24	4	28.6	12	1 R78578	LACI K1 derivative
25	4	28.6	12	1 R96443	Hepatitis C virus
26	4	28.6	12	1 R96444	Hepatitis C virus
27	4	28.6	13	1 R67073	Clot-inducing pept
28	4	28.6	14	1 W21535	Prorenin derived s
29	4	28.6	14	1 W21536	Prorenin derived s
30	4	28.6	15	1 R26578	Retro-peptide. New
31	4	28.6	15	1 W50991	Snake venom lopus
32	4	28.6	15	1 W50990	Snake venom lopus
33	4	28.6	15	1 W50992	Snake venom lopus

Peptide which bind
Snake venom derive
Vasopressin type 2
Amino acid sequenc
N-terminal sequenc
H. horridum extendi
Human B-type natri
N-terminal sequenc
Snake venom derive
Human 5' EST secre
UGT1BP Exon 1 prod
Transcriptional si

ALIGNMENTS

RESULT 1
ID W35340 standard; peptide; 14 AA.
AC W35340;
DC 17-APR-1998 (first entry)
DE Human acetylcholinesterase 14-mer peptide.
KW Acetylcholinesterase; AChE; neuronal degeneration;
KW Parkinson's disease; Alzheimer's disease; stroke; cancer;
KW calcium channel modulator; antibody; inhibitor.
OS Homo sapiens.
PN W09735962-AL.
PD 02-OCT-1997; G00796.
PF 21-MAR-1997; G00796.
PR 22-MAR-1996; GB-006040.
PA (ISIS-) ISIS INNOVATION LTD.
PI Greenfield SA, Vaux DU;
DR WPI: 97-489626/45.
PT Peptide(s) from acetylcholine esterase which open calcium channels -
PT used for treating disorders of the central nervous system, cancer
PT and stroke
PS Claim 1; Page 20; 27pp; English.
CC This 14-mer peptide corresponds to residues 535-548 of the
CC Acetylcholinesterase mature protein. This peptide is known to
CC act alone or in synergism with a fragment of beta-amyloid to
CC contribute to neuronal degeneration. Compounds that inhibit the
CC biological activity of the novel peptides, and antibodies, can be
CC used to control cytoplasmic calcium ion currents in vivo, and are
CC useful for treating disorders of the central nervous system
CC (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.
SQ Sequence 14 AA;

Query Match 100.0%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.6e-11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
DB 1 AEFHRWSSYVHWK 14

RPEP

RESULT 2
ID R77010 standard; Protein; 39 AA.
AC R77010;
DC 31-MAR-1996 (first entry)
DE Alternative human acetylcholinesterase (ACHE) protein.
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;
KW Chromosome-2q22; acetylcholine-hydrolyzing enzyme.
OS Homo sapiens.
PN W09523158-AL.
PD 31-AUG-1995;
PF 28-FEB-1995; U02806.
PR 28-FEB-1994; US-202755;
PR 09-JAN-1993; US-370156.
PA (KOHN/) KOHN K I.

PA (YISS) YISSUM RES & DEV CO.
 PI Shani M, Soreq H, Zakut H;
 DR WPI; 95-311499/40.
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -
 PT expressed in transgenic animal assay system for evaluating anti-ChE
 PT activity of organo-phosphate(s), etc. Or as model of ChE imbalance
 PS Disclosure; Fig.6; 55pp; English.
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at
 CC neuromuscular junctions where it serves a vital function in
 CC modulating cholinergic neurotransmission. This alternatively
 CC spliced form of human AChE may be expressed in transgenic animals
 CC which are used in an assay system for determining the anti-ChE
 CC activity of organophosphates, carbamates, anti-ChE drugs, plant
 CC glycoalkaloids and snake venoms.
 SQ Sequence 39 AA;

Query Match 100.0%; Score 14; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
 | | | | | | | | | | | | | | | | | |
 Db 11 AEFHRWSSVMVHWK 24

RESULT 3
 ID W48800 standard; protein; 45 AA.
 AC W48800;
 DT 07-OCT-1998 (first entry)
 DE C-terminal fragment of human acetylcholine esterase variant El-4.6.
 KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;
 KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;
 KW chemotherapeutic drug; central nervous system.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT Region 1..5
 FT /note= "This region is encoded by the 3' end of
 FT AChE exon 4"

FT Region 5..45
 FT /note= "Residues encoded by AChE exon 6"
 FT W09822132-A2.
 PD 28-MAY-1998.
 PR 20-NOV-1997; U21696.
 PR 21-JUL-1997; US-0533200.
 PR 20-NOV-1996; US-031194.
 PR 12-DEC-1996; US-035266.
 PA (KOHN/) KOHN K I.
 PA (YISS) YISSUM RES & DEV CO.
 PI Friedman A, Kaufman S, Soreq H;
 DR WPI; 98-312172/27.
 PT Increasing the permeability of the blood/brain barrier - using e.g.
 PT adrenaline, atropine or acetylcholine esterase I4 splice variant.
 PT peptide, useful for imaging and/or treatment of central nervous
 PT system disorders
 PS Disclosure; Fig 2; 71pp; English.

CC The present sequence represents a C-terminal fragment of the human
 CC acetylcholine esterase splice variant El-4.6. The AChE El-4.6 variant
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues
 CC encoded by the alternatively spliced AChE exon 6. The invention claims
 CC for the human acetylcholine esterase-I4 (AChE-I4) readthrough splice
 CC variant (W48797). The invention provides a pharmaceutical composition,
 CC for facilitating passage of compounds through the blood/brain barrier.
 CC (BBB), comprising of AChE-I4, I4 peptide (see W48797) or AChE-I4,
 CC analogues (such as the AChE El-4.6 variant) together with a
 CC pharmaceutically acceptable carrier. The pharmaceutical composition
 CC is claimed to facilitate a reversible disruption of the BBB allowing
 CC transport of compounds through the BBB. The compounds, e.g. imaging
 CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful
 CC for the diagnosis and treatment of diseases or disorders of the CNS such
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc.
 SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
 | | | | | | | | | | | | | | | | | |
 Db 17 AEFHRWSSVMVHWK 30

RESULT 4
 ID W68144 standard; Protein; 45 AA.
 AC W68144;
 DT 05-OCT-1998 (first entry)

DE Human AChE splice variant El-4, 6.
 KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis;
 KW Alzheimer's disease; Alzheimer's disease; central nervous system;
 KW neuromuscular junction; cholinergic signalling; brain.
 OS Homo sapiens.

PN W09826062-A2.
 PD 18-JUN-1998.
 PR 12-DEC-1997; U23598.
 PR 21-JUL-1997; US-053334.
 PR 12-DEC-1996; US-035266.
 PR 13-FEB-1997; US-037777.
 PR 02-MAY-1997; US-850347.
 PA (KOHN/) KOHN K I.

PA (YISS) YISSUM RES & DEV CO.
 PI Eckstein F, Friedman A, Kaufman S, Soreq H;
 DR WPI; 98-348522/30.
 PT Synthetic nuclease resistant antisense oligodeoxynucleotides -
 PT directed against acetylcholinesterase, useful for treating
 PT Parkinson's and Alzheimer's diseases and myasthenia gravis
 PS Disclosure; Fig 12; 89pp; English.

CC This represents the amino acid sequence of a human acetylcholinesterase
 CC (AChE) splice variant. The invention provides sequences shown in V41278
 CC to V41285 that represent synthetic nuclease resistant antisense
 CC oligodeoxynucleotides which are capable of selectively modulating human
 CC acetylcholinesterase (AChE) production. These oligonucleotides are
 CC targeted to a splice junction in a splice variant of AChE mRNA and are
 CC capable of selectively modulating human AChE production in the central
 CC nervous system and neuromuscular junction. The invention also provides a
 CC method for determining the efficacy of these human AChE specific
 CC antisense oligonucleotides. These antisense oligonucleotides can be used
 CC to restore balanced cholinergic signalling in the brain, particularly
 CC related to learning and memory as well as stress disorders, Parkinson's
 CC and Alzheimer's disease. They can also be used to reduce production of
 CC therefore deposition of AChE in the neuromuscular junctions of patients
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low
 CC doses while avoiding many of the side effects associated with Tacrine and
 CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and
 CC related drugs for myasthenia gravis.
 SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.2e-10;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
 | | | | | | | | | | | | | | | | | |
 Db 17 AEFHRWSSVMVHWK 30

RESULT 5
 ID W74586 standard; Protein; 45 AA.
 AC W74586;
 DT 21-DEC-1998 (first entry)

DE Amino acid sequence of the human AChE variant 1.
 KW Nuclease resistance; inhibition; human; acetylcholinesterase; AChE;

KW Central nervous system; CNS.
OS Homo sapiens.
PN WO9839486-A1.
PD 11-SEP-1998.
PR 06-MAR-1998; 004503.
PR 06-MAR-1998; US-040203.
PA (KOHN) KOHN K I.
PA (YISS) YISSUM RES & DEV CO.
PI Seidman S, Shohami E, Soreq H;
DR WPI; 98-506377/43.
PT Treatment of injury to central nervous system - by administration of
PT inhibitor of acetylcholinesterase production
PS Disclosure; Page 61; 89pp; English.
CC This is the amino acid sequence of a human acetylcholinesterase
CC (AChE) variant used in the method of the invention, where inhibitors
CC of AChE are used to treat injury to the central nervous system (CNS).
CC The AChE inhibitor can also be used to facilitate transplantation of
CC neuronal cells to the CNS of a patient. The inhibitor can also be
CC used to improve hippocampal neuron survival following injury to the
CC CNS. The CNS injuries that can be treated with the method include
CC epilepsy, stroke, Huntington's disease, head injury, spinal injury,
CC pain, Parkinson's disease, myelin deficiencies, neuromuscular
CC disorders, neurological pain, amyotrophic lateral sclerosis,
CC Alzheimer's disease, and affective disorders of the brain.
SQ Sequence 45 AA;

Query Match 100.0%; Score 14; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
DB 17 AEFHRWSSYVHWK 30
|||||
RESULT 6
R06990
ID R06990 standard; protein; 500 AA.
AC R06990;
DT 16-JAN-1991 (first entry)
DE Human foetal acetylcholinesterase (hAChE) primary transcript.
KW Organophosphorous poisoning; OP; cancer; leukaemia;
KW megakaryocytopenia; ovarian cancer.
OS Homo sapiens.
PN EP-388906-A.
PD 26-SEP-1990.
PR 20-MAR-1990; 105274.
PA (YISS) YISSUM RES & DEV CO.
PI Soreq H, Zakut H;
DR N-PSDB; Q05999.
PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
PT cytopoietic disorders and ovarian carcinomas.
PS Disclosure; Fig 1c; 47pp; English.
CC Gene product is useful as an active pharmacological component for the
CC prophylaxis and treatment of organophosphorous poisoning, and post-
CC surgical apnea due to succinylcholine administration.
CC cDNA probe to the sequence may be used in diagnosis of various
CC leukaemias, abnormal megakaryocytopenia and ovarian carcinomas.
SQ Sequence 500 AA;

Query Match 100.0%; Score 14; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
DB 472 AEFHRWSSYVHWK 485
|||||
RESULT 6
R06990
ID R06990 standard; protein; 500 AA.
AC R06990;
DT 16-JAN-1991 (first entry)
DE Human foetal acetylcholinesterase (hAChE) primary transcript.
KW Organophosphorous poisoning; OP; cancer; leukaemia;
KW megakaryocytopenia; ovarian cancer.
OS Homo sapiens.
PN EP-388906-A.
PD 26-SEP-1990.
PR 20-MAR-1990; 105274.
PA (YISS) YISSUM RES & DEV CO.
PI Soreq H, Zakut H;
DR N-PSDB; Q05999.
PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
PT cytopoietic disorders and ovarian carcinomas.
PS Disclosure; Fig 1c; 47pp; English.
CC Gene product is useful as an active pharmacological component for the
CC prophylaxis and treatment of organophosphorous poisoning, and post-
CC surgical apnea due to succinylcholine administration.
CC cDNA probe to the sequence may be used in diagnosis of various
CC leukaemias, abnormal megakaryocytopenia and ovarian carcinomas.
SQ Sequence 500 AA;

Query Match 100.0%; Score 14; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
DB 472 AEFHRWSSYVHWK 485
|||||

RESULT 7
R06989
ID R06989 standard; protein; 613 AA.
AC R06989;
DT 16-JAN-1991 (first entry)
DE Human acetylcholinesterase (hAChE) primary transcript.
KW Organophosphorous poisoning; OP; cancer; leukaemia;
KW megakaryocytopenia; ovarian cancer.
OS Homo sapiens.
PN EP-388906-A.
PD 26-SEP-1990.
PR 20-MAR-1990; 105274.
PA (YISS) YISSUM RES & DEV CO.
PI Soreq H, Zakut H;
DR N-PSDB; Q05998.
PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
PT cytopoietic disorders and ovarian carcinomas.
PS Claim 5; Page 25; 47pp; English.
CC Gene product is useful as an active pharmacological component for the
CC prophylaxis and treatment of organophosphorous poisoning, and post-
CC surgical apnea due to succinylcholine administration.
CC cDNA probe to the sequence may be used in diagnosis of various
CC leukaemias, abnormal megakaryocytopenia and ovarian carcinomas.
SQ Sequence 613 AA;

Query Match 100.0%; Score 14; DB 1; Length 613;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
DB 585 AEFHRWSSYVHWK 598
|||||

RESULT 8
R0726
ID R0726 standard; protein; 614 AA.
AC R0726;
DT 31-MAR-1996 (first entry)
DE Human acetylcholinesterase (AChE) protein.
KW Acetylcholinesterase; acetylcholinesterase; EC-3.1.1.7;
KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.
OS Homo sapiens.
PN WO9523158-A1.
PD 31-AUG-1995.
PR 28-FEB-1995; 002806.
PR 28-FEB-1994; US-202755.
PR 09-JAN-1995; US-370156.
PA (KOHN) KOHN K I.
PA (YISS) YISSUM RES & DEV CO.
PI Shani M, Soreq H, Zakut H;
DR WPI; 95-314499/40.
DR N-PSDB; Q99002.
PT Alternative forms of human acetylcholinesterase (ChE) gene -
PT expressed in transgenic animal assay system for evaluating anti-ChE
PT activity of organo-phosphate(s), etc. or as model of ChE imbalance
PS Claim 3; Fig.18; 55pp; English.
CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at
CC neuromuscular junctions where it serves a vital function in
CC modulating cholinergic neurotransmission. Alternatively spliced
CC forms of human AChE may be expressed in transgenic animals which
CC are used in an assay system for determining the anti-ChE activity
CC of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids
CC and snake venoms.
SQ Sequence 614 AA;

Query Match 100.0%; Score 14; DB 1; Length 614;
QY 1 AEFHRWSSYVHWK 14
DB 585 AEFHRWSSYVHWK 598
|||||

Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
DB 586 AEFHRWSSYVHWK 599
|||||

RESULT 9

W39078 ID W39078 standard; protein; 575 AA.
AC W39078

DT 08-APR-1998 (first entry)
DE Torpedo californica acetylcholinesterase AChE.
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;
OS ray: chemical agent; treatment; prevention; aging; mutant.
FH Torpedo californica.

Key Location/Qualifiers

FT Region 67..94
FT /note= "region as indicated in specification."
FT Modified_site 59..61
FT /note= "site as indicated in specification"
FT Region 254..265
FT /note= "region as indicated in specification"
FT Region 402..521
FT /note= "region as indicated in specification"
FT Modified_site 416..418
FT /note= "site as indicated in specification"
FT Modified_site 457..459
FT /note= "site as indicated in specification"
FT Modified_site 569..571
FT /note= "site as indicated in specification"

US5695750-A.

PD 09-DEC-1997.

PF 25-NOV-1994; 348920.

PR 25-NOV-1994; US-348920.

PI (USSA) US SEC OF ARMY.

PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;

DR WPI; 98-041233/04.

PT Mutant Torpedo acetylcholinesterase - useful for detoxifying

PT organo-phosphate compounds

PS Disclosure; Fig 1; 12pp; English.

CC This sequence represents an acetylcholinesterase (AChE) from Torpedo
CC californica which is used to create enzymes capable of detoxifying
CC organophosphates. Mutant versions of this AChE are useful when combined
CC with an oxime for detoxifying chemical warfare agents such as sarin or as
CC a means of treating or preventing the deleterious effects of
CC organophosphate exposure in organisms. Such variants can also destroy
CC organophosphates in an environmentally friendly manner and be more
CC resistant to aging than wild-type enzymes.

Sequence 575 AA;

Query Match

Best Local Similarity 64.3%; Score 9; DB 1; Length 575;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRHWSSY 10

DB 548 EFRHWSSY 556

|||||

RESULT 10

W39079 ID W39079 standard; protein; 575 AA.
AC W39079

DT 08-APR-1998 (first entry)

DE Torpedo californica acetylcholinesterase AChE mutant E1990.

KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;

OS ray: chemical agent; treatment; prevention; aging; mutant.

OS Torpedo californica.

OS Synthetic.

FH Key

Location/Qualifiers

FT Modified_site 59..61
FT /note= "site as indicated in specification"
FT Region 67..94
FT /note= "region as indicated in specification"
FT Modified_site 199
FT /label= E1990
FT /note= "wild-type Glu is replaced by Gln"
FT Region 254..265
FT /note= "region as given in specification"
FT Region 402..521
FT /note= "region as given in specification"
FT Modified_site 416..418
FT /note= "site as given in specification"
FT Modified_site 457..459
FT /note= "site as given in specification"
FT Modified_site 533..535
FT /note= "site as given in specification"

US5695750-A.

PD 09-DEC-1997.

PF 25-NOV-1994; 348920.

PR 25-NOV-1994; US-348920.

PI (USSA) US SEC OF ARMY.

PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;

DR WPI; 98-041233/04.

PT Mutant Torpedo acetylcholinesterase - useful for detoxifying

PT organo-phosphate compounds

PS Claim 1; Fig 2; 12pp; English.

CC This sequence represents a variant of the enzyme acetylcholinesterase
CC (AChE) from Torpedo californica which is capable of detoxifying
CC organophosphates. This E1990 mutant has greater resistance to aging
CC than the wild-type AChE and can destroy organophosphates in an
CC environmentally friendly manner. When combined with an oxime, this
CC mutant's ability to detoxify several organophosphates is amplified
CC and is predicted to have applications for the detoxification of chemical
CC warfare agents such as sarin or as a means of treating or preventing the
CC deleterious effects of organophosphate exposure in organisms.

Sequence 575 AA;

Query Match

Best Local Similarity 64.3%; Score 9; DB 1; Length 575;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRHWSSY 10

DB 548 EFRHWSSY 556

|||||

RESULT 11

R63398

ID R63398 standard; Protein; 12 AA.

AC R63398;

DT 09-AUG-1995 (first entry)

DE Peptide fragment of V1 region of hepatitis C virus.

KW Hepatitis C virus; HCV; primer; probe; detection; diagnosis;

KW classification; immunisation; prophylaxis; serotyping.

OS Hepatitis C virus.

PN W09425601-A.

PD 10-NOV-1994.

PF 27-APR-1994; E01323.

PR 27-APR-1993; EP-401099.

PR 05-AUG-1993; EP-402019.

PI (INNO-) INNOGENETICS NV SA.

PI Maertens G, Stuyver L;

DR WPI; 94-358277/44.

PT New polynucleotide sequences from hepatitis C virus - and related
PT vectors, polypeptide(s) and antibodies, useful for immunisation,
PT treatment, diagnosis and typing of HCV isolates

PS Claim 15; Page 277; 404pp; English

CC Compositions comprising at least 5, and pref. 8 or more contiguous

CC nucleotides selected from an HCV type 3 genomic sequence, more

CC particularly (i) the region spanning positions 417-957 of the

CC Core/E1 region of HCV subtype 3a; (ii) the region spanning positions

CC 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning
 CC positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the
 CC region spanning positions 8023-8235 of the NS5 region of the BR36
 CC subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic
 CC sequence, or, from a subtype 2d genomic sequence, a type 4 genomic
 CC sequence; or the coding region of subtype 5a, may be used as primers
 CC to amplify nucleic acid from an isolate belonging to a specific
 CC genotype, or as a probe for specific detection/classification of
 CC nucleic acid. Polypeptides encoded by the nucleotides in such
 CC compositions may be used for immunisation against HCV, for the
 CC detection of antibodies directed against HCV and for serotyping.
 CC This polypeptide corresponds to positions 192-203 of the VI region
 CC of HCV.
 SQ Sequence 12 AA;

Query Match 35.7%; Score 5; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVNV 11

Db 8 SSVNV 12

RESULT 12

W61227
 ID W61227 standard; Protein; 111 AA.
 AC W61227;
 DT 02-OCT-1998 (first entry)
 DE Streptococcus pneumoniae Sp102 protein.
 KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
 KW detection; pneumonia; otitis media; meningitis.
 OS Streptococcus pneumoniae.
 PN W61227-1998-02.
 PD 07-MAY-1998.
 PF 30-OCT-1997; U19422.
 PR 31-OCT-1996; US-029960.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
 DR WPI: 98-272224/24.
 DR N-PSDB; V27413.
 DT Nucleic acid encoding antigenic peptide(s) from Streptococcus
 PT pneumoniae - or their epitope-containing fragments, useful in
 PT protective or therapeutic vaccines, and for diagnosis
 PS Claim 11; Page 85; 118pp; English.
 CC The present sequence represents a protein from Streptococcus pneumoniae.
 CC The nucleic acid sequence encoding the Streptococcus pneumoniae protein
 CC can be useful in vaccines for inducing protective antibodies against
 CC Streptococcus pneumoniae, for treatment or prevention of infection e.g.
 CC pneumonia, otitis media or meningitis. Probes based on the nucleic acid
 CC are used to detect Streptococcus infection (by usual hybridisation or
 CC amplification methods), also for isolating Streptococcus genes or their
 CC allelic variants. The protein can be used similarly to detect specific
 CC antibodies in standard immunoassays, especially for diagnosing or
 CC monitoring infections. Antibodies which bind the protein are used to
 CC detect corresponding antigens, to purify the protein and for passive
 CC immunisation (optionally coupled to a toxin). Vaccines are administered,
 CC e.g. by injection, orally or through the skin, typically at 0.01-1000
 CC (especially 10-300) mu g/ml per dose.
 SQ Sequence 111 AA;

Query Match 35.7%; Score 5; DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5

Db 37 AEFHR 41

RESULT 13

W74955
 ID W74955 standard; Protein; 136 AA.
 AC W74955;
 DT 25-JAN-1999 (first entry)
 DE Human secreted protein encoded by gene 77 clone HOEAS24.
 KW Human; secreted protein; testis; tumour; foetal brain tissue;
 KW fusion protein; cancer; central nervous system; seizure;
 KW diagnosis; neurodegenerative disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 136 /label= unknown
 FT W09839448-A2.
 PN 11-SEP-1998.
 PD 06-MAR-1998; U04493.
 PF 02-OCT-1997; US-061060.
 PR 07-MAR-1997; US-038621.
 PR 07-MAR-1997; US-040161.
 PR 07-MAR-1997; US-040162.
 PR 07-MAR-1997; US-040163.
 PR 07-MAR-1997; US-040333.
 PR 07-MAR-1997; US-040334.
 PR 07-MAR-1997; US-040336.
 PR 07-MAR-1997; US-040626.
 PR 11-APR-1997; US-043311.
 PR 11-APR-1997; US-043312.
 PR 11-APR-1997; US-043313.
 PR 11-APR-1997; US-043314.
 PR 11-APR-1997; US-043568.
 PR 11-APR-1997; US-043569.
 PR 11-APR-1997; US-043576.
 PR 11-APR-1997; US-043578.
 PR 11-APR-1997; US-043580.
 PR 11-APR-1997; US-043669.
 PR 11-APR-1997; US-043670.
 PR 11-APR-1997; US-043671.
 PR 11-APR-1997; US-043672.
 PR 11-APR-1997; US-043674.
 PR 23-MAY-1997; US-047492.
 PR 23-MAY-1997; US-047500.
 PR 23-MAY-1997; US-047501.
 PR 23-MAY-1997; US-047502.
 PR 23-MAY-1997; US-047503.
 PR 23-MAY-1997; US-047504.
 PR 23-MAY-1997; US-047582.
 PR 23-MAY-1997; US-047583.
 PR 23-MAY-1997; US-047584.
 PR 23-MAY-1997; US-047585.
 PR 23-MAY-1997; US-047586.
 PR 23-MAY-1997; US-047587.
 PR 23-MAY-1997; US-047588.
 PR 23-MAY-1997; US-047589.
 PR 23-MAY-1997; US-047590.
 PR 23-MAY-1997; US-047592.
 PR 23-MAY-1997; US-047593.
 PR 23-MAY-1997; US-047594.
 PR 23-MAY-1997; US-047595.
 PR 23-MAY-1997; US-047596.
 PR 23-MAY-1997; US-047597.
 PR 23-MAY-1997; US-047598.
 PR 23-MAY-1997; US-047599.
 PR 23-MAY-1997; US-047600.
 PR 23-MAY-1997; US-047601.
 PR 23-MAY-1997; US-047612.
 PR 23-MAY-1997; US-047613.
 PR 23-MAY-1997; US-047614.
 PR 23-MAY-1997; US-047615.
 PR 23-MAY-1997; US-047617.
 PR 23-MAY-1997; US-047618.
 PR 23-MAY-1997; US-047632.
 PR 23-MAY-1997; US-047633.
 PR 06-JUN-1997; US-048964.
 PR 06-JUN-1997; US-048974.

PR 13-JUN-1997; US-049610.
 PR 08-JUL-1997; US-051926.
 PR 16-JUL-1997; US-052874.
 PR 18-AUG-1997; US-055724.
 PR 22-AUG-1997; US-056630.
 PR 22-AUG-1997; US-056631.
 PR 22-AUG-1997; US-056632.
 PR 22-AUG-1997; US-056636.
 PR 22-AUG-1997; US-056637.
 PR 22-AUG-1997; US-056662.
 PR 22-AUG-1997; US-056664.
 PR 22-AUG-1997; US-056845.
 PR 22-AUG-1997; US-056862.
 PR 22-AUG-1997; US-056864.
 PR 22-AUG-1997; US-056872.
 PR 22-AUG-1997; US-056874.
 PR 22-AUG-1997; US-056875.
 PR 22-AUG-1997; US-056876.
 PR 22-AUG-1997; US-056877.
 PR 22-AUG-1997; US-056878.
 PR 22-AUG-1997; US-056879.
 PR 22-AUG-1997; US-056880.
 PR 22-AUG-1997; US-056881.
 PR 22-AUG-1997; US-056882.
 PR 22-AUG-1997; US-056884.
 PR 22-AUG-1997; US-056886.
 PR 22-AUG-1997; US-056887.
 PR 22-AUG-1997; US-056888.
 PR 22-AUG-1997; US-056889.
 PR 22-AUG-1997; US-056892.
 PR 22-AUG-1997; US-056893.
 PR 22-AUG-1997; US-056894.
 PR 22-AUG-1997; US-056903.
 PR 22-AUG-1997; US-056908.
 PR 22-AUG-1997; US-056909.
 PR 22-AUG-1997; US-056910.
 PR 22-AUG-1997; US-056911.
 PR 05-SEP-1997; US-057650.
 PR 05-SEP-1997; US-057669.
 PR 05-SEP-1997; US-057761.
 PR 12-SEP-1997; US-058785.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 DR WPI: 98-506364/43.
 DR N-PSDB: V59740.
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS Claim 1; Page 672; 721pp; English.
 CC This sequence represents a secreted human protein encoded by the nucleic
 CC acid molecule designated Gene 77 from the human cDNA clone HOEAS24
 CC (deposited as clone ATCC 97900 and ATCC 209046).
 CC The gene can be used to generate fusion proteins by linking to the gene
 CC to a human immunoglobulin FC portion (e.g. V59502) for increasing the
 CC stability of the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: V59511-V59812; amino acid sequences W74731-W75036) which
 CC are useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. Also, pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 186 polynucleotides, based on
 CC which tissues they are most highly expressed in (see V59511 for described
 CC uses).
 SQ Sequence 136 AA;

Query Match 35.7%; Score 5; DB 1; Length 136;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSMV 11
 |||||
 Db 33 SSMV 37

RESULT 14

P70559
 ID P70559 standard; Protein; 256 AA.
 AC P70559;
 DT 30-APR-1991 (first entry)
 DE Product of ORF 1 from MiMV strand (a).
 KW Geminivirus.
 OS Mungbean yellow mosaic virus.
 PN J62126982-A.
 PD 09-JUN-1987; 266080.
 PF 28-NOV-1985; JP-266080.
 PR WPI: 87-196308/28.
 PA (TEIJ) TEIJIN KK.
 DR N-PSDB: N70892.
 PT Novel DNA and hybrid DNA useful - as vector for recombinant work
 PT of plant gene.
 PS Disclosure; Fig 5; 21pp; Japanese.
 CC The sequence is encoded by ORF 1 which occurs on the positive
 CC strand of the (a) molecule of the geminivirus.
 CC See also P70560-P70567
 SQ Sequence 256 AA;

Query Match 35.7%; Score 5; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HRWS 8
 |||||
 Db 19 HRWS 23

RESULT 15

R63805
 ID R63805 standard; Protein; 261 AA.
 AC R63805;
 DT 07-DEC-1994 (first entry)
 DE Polyhydroxyalkanoate decomposing activity polypeptide.
 KW Polyhydroxyalkanoate decomposing enzyme; PHA.
 OS Zoogloea ramigera.
 PN J06086681-A.
 PD 29-MAR-1994; 279099.
 PF 07-SEP-1992; JP-279099.
 PR 07-SEP-1992; JP-279099.
 PA (ELED) DENKI KAGAKU KOGYO KK.
 PA (UYKA-) GH KANAGAWA DAIGAKU.
 PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
 DR WPI: 94-140539/17.
 DR N-PSDB: Q63879.
 PT DNA encoding poly-hydroxy-alkanoate decomposing enzyme - useful
 PT for preparing poly-hydroxy-alkanoate in large quantities
 PS Claim 3; Page 13-14; 15pp; Japanese.
 CC R63805 is encoded by ORF 2 of Q63789, which produces a polypeptide
 CC which shows polyhydroxyalkanoate decomposing activity. The method
 CC used allows the polypeptide to be prepared in large quantities.
 SQ Sequence 261 AA;

Query Match 35.7%; Score 5; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5
 |||||
 Db 84 AEFHR 88

Wed Sep 13 08:11:25 2000

us-09-155-076-1.rag

Page 7

Search completed: September 13, 2000, 02:25:00
Job time: 173 sec

Wed Sep 13 08:11:29 2000

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:38 ; Search time 22.46 Seconds
(without alignments)
43.218 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 14
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0 225878

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL.12.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	611	6	O62763 felis silve
2	10	71.4	633	13	O42275 electrophor
3	9	64.3	95	13	Q9w6y8 torpedo cal
4	6	42.9	469	2	P73738 synchocyst
5	5	35.7	149	12	Q81753 hepatitis c
6	5	35.7	193	12	Q81558 hepatitis c
7	5	35.7	219	8	Q9XQU7
8	5	35.7	235	13	Q9W7Q8
9	5	35.7	244	12	P88361 human immun
10	5	35.7	251	12	P88358 human immun
11	5	35.7	255	5	Q22117 caenorhabdi
12	5	35.7	262	12	O10441 mouse adeno
13	5	35.7	263	6	O97972 oryctolagus
14	5	35.7	285	2	Q52970 rhizobium m
15	5	35.7	294	8	Q9XMG3 epichloe ty
16	5	35.7	318	12	Q98691 hepatitis c
17	5	35.7	319	12	Q81557 hepatitis c
18	5	35.7	335	1	O29464 archaeoglob
19	5	35.7	339	2	O32123 bacillus su

Q9zvp5 arabidopsis
O16472 caenorhabdi
O83906 treponema p
O24322 phaseolus v
Q9zvt5 arabidopsis
O15679 leishmania
O18710 leishmania
O18713 leishmania
O77439 leishmania
O23853 brassica ca
O80346 raphanus sa
O23033 arabidopsis
O23852 brassica ca
Q93795 caenorhabdi
O15322 homo sapien
Q9zak2 anabaena va
O13601 schizosacch
O68307 nostoc poc7
O44216 anabaena sp
O61745 caenorhabdi
Q95779 synchocyst
Q9xsb8 canis famill
O18097 caenorhabdi
O18044 drosophila
Q96fp3 chlamydia p
O13858 schizosacch

ALIGNMENTS

RESULT 1
O62763 PRELIMINARY; PRT; 611 AA.
AC O62763;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ACETYLCHOLINESTERASE COLLAGEN-TAILED OR GLOBULAR FORM PRECURSOR.
GN ACHE.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
RN [1]
RP SEQUENCE FROM N.A.
RA BARTELS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053485; AAC08995.1; -
DR HSSP; P22303; 2CLJ.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
SQ SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

Query Match 100.0%; Score 14; DB 6; Length 611;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
DB 583 AEFHRWSSVMVHWK 596

RESULT 2
O42275 PRELIMINARY; PRT; 633 AA.
ID O42275;
AC O42275;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ACETYLCHOLINESTERASE CATALYTIC SUBUNIT PRECURSOR (EC 3.1.1.7).

OS Electrophorus electricus (Electric eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;
 OC Gymnotidae; Electrophoridae; Electrophorus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SIMON S., MASSOULIE J.;
 RL J. Biol. Chem. 0:0-0(1997).
 DR EMBL; AF030422; AAB86606.1; -.
 DR HSP; P04058; 1ACU.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PFAM; PF00135; Coesterase; 2.
 DR PRINTS; PR00878; CHOLINESTERASE.
 KW Signal; Hydrolase.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 633 POTENTIAL.
 SQ SEQUENCE 633 AA; 71814 MW; 6050AB05 CRC32;

Query Match 71.4%; Score 10; DB 13; Length 633;
 Best Local Similarity 100.0%; Pred. No. 8e-06;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSYM 10
 |||||
 Db 605 AEFHRSSYM 614

RESULT 3
 Q9W6Y8 PRELIMINARY; PRT; 95 AA.
 ID Q9W6Y8
 AC Q9W6Y8
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE ACETYLCOLINESTERASE (FRAGMENT).
 OS Torpedo californica (Pacific electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MAULET Y., CAMP S., GIBNEY G., RACHINSKY T.L., EKSTROM T.J.,
 RA TAYLOR P.;
 RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X56517; CAB37951.1; -.
 DR EMBL; X56516; CAB37951.1; JOINED.
 FT NON_TER 1
 SQ SEQUENCE 95 AA; 11752 MW; F7387712 CRC32;

Query Match 64.3%; Score 9; DB 13; Length 95;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRHRSSYM 10
 |||||
 Db 68 EFRHRSSYM 76

RESULT 4
 P73738 PRELIMINARY; PRT; 469 AA.
 ID P73738
 AC P73738
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE HYPOTHETICAL 52.5 KD PROTEIN.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;

RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NAROO K., OKUMURA S.,
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res 3:109-136(1996).
 DR EMBL; D90909; BAAL7786.1; -.
 DR PFAM; PF00355; Rieske; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 469 AA; 52544 MW; 0887A65E CRC32;

Query Match 42.9%; Score 6; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRW 6
 |||||
 Db 349 AEFHRW 354

RESULT 5
 Q81753 PRELIMINARY; PRT; 149 AA.
 ID Q81753
 AC Q81753
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
 DE PRECURSOR PROTEIN (FRAGMENTS).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepatitis C-like viruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95052487.
 RA VAN DOORN L.J., KLETER B., STUYVER L., MAERTENS G., BROUWER H.,
 RA SCHALM S., HEIJTINK R., QUINT W.;
 RT "Analysis of hepatitis C virus genotypes by a line probe assay and
 RT correlation with antibody profiles.";
 RL J. Hepatol. 21:122-129(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA VAN DOORN L.J., KLETER B.G.E.M., STUYVER L., MAERTENS G.,
 RA BROUWER J.T., SCHALM S.W., HEIJTINK R.A., QUINT W.G.V.;
 RL J. Gen. Virol. 0:0-0(0).
 DR EMBL; L39294; AAA67817.1; -.
 DR PFAM; PF01542; HCV_core; 1.
 DR PFAM; PF01539; HCV_env; 1.
 FT NON_TER 1
 FT CHAIN 1 >32 CORE PROTEIN.
 FT NON_CONS 32 33
 FT CHAIN 33 >149 E1 PROTEIN.
 FT NON_TER 149 149
 SQ SEQUENCE 149 AA; 15854 MW; EB9593D2 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 149;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11
 |||||
 Db 40 SSYMV 44

RESULT 6
Q81558 PRELIMINARY; PRT; 193 AA.
AC Q81558;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE (NE92) CORE PROTEIN (FRAGMENTS).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepatitis C-like viruses.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NE92;
RC MEDLINE; 95023999.
RX STUYVER L., VAN ARNHEM W., WYSEUR A., HERNANDEZ F., DELAPORTE E.,
RA MAERTENS G.;
RA "Classification of hepatitis C viruses based on phylogenetic analysis
of the envelope 1 and nonstructural 5B regions and identification of
five additional subtypes.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:10134-10138(1994).
RL EMBL; L29633; AAA65816.1; -;
DR PFAM; PF01542; HCV_core; 1.
DR PFAM; PF01539; HCV_env; 1.
KW Envelope protein.
FT NON_TER 1
FT CHAIN 1
FT NON_CONS 65
FT CHAIN 66
FT CHAIN 66
FT CHAIN >193
FT NON_TER 193
SQ SEQUENCE 193 AA; 20460 MW; 9FOAD762 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 193;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYM 11
Db 73 SSYM 77

RESULT 7
Q9XQ07 PRELIMINARY; PRT; 219 AA.
AC Q9XQ07;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYTOCHROME B6.
GN PETB.
OS Heterocapsa triquetra.
OG Chloroplast.
OC Eukaryota; Alveolata; Dinophyceae; Peridiniales; Heterocapsaceae;
OC Heterocapsa.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCMP 449;
RX MEDLINE; 99334925.
RA ZHANG Z., GREEN B.R., CAVALIER-SMITH T.;
RT "Single gene circles in dinoflagellate chloroplast genomes.";
RL Nature 400:155-159(1999).
DR EMBL; AF130037; AD44704.1; -;
KW Chloroplast.
SQ SEQUENCE 219 AA; 24373 MW; 9CIA3172 CRC32;

Query Match 35.7%; Score 5; DB 8; Length 219;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HRWS 8

Db 86 HRWS 90
|||||
RESULT 8
Q9W7Q8 PRELIMINARY; PRT; 235 AA.
AC Q9W7Q8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HOXD-4.
GN HOXD-4.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Pleuronectiformes; Pleuronectoidae; Bothidae; Paralicthys.
RN [1]
RN SEQUENCE FROM N.A.
RP SUZUKI T., OOHARA I., KUROKAWA T.;
RT "Hoxd-4 expression during pharyngeal arch development in flounder
(Paralicthys olivaceus) embryos and effects of retinoic acid on
expression.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE; 98277852.
RX SUZUKI T., OOHARA I., KUROKAWA T.;
RT "Hoxd-4 expression during pharyngeal arch development in flounder
(Paralicthys olivaceus) embryos and effects of retinoic acid on
expression.";
RL Zool. Sci. 15:57-67(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AB029749; BAA82361.1; -;
DR PROSITE; PS00027; HOMEBOX.1; 1.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 235 AA; 27101 MW; 57A1C75E CRC32;

Query Match 35.7%; Score 5; DB 13; Length 235;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYM 11
Db 4 SSYM 8
|||||
RESULT 9
P88361 PRELIMINARY; PRT; 244 AA.
AC P88361;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Lentivirus.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=PATIENT H;
RX MEDLINE; 97184515.
RA McDONALD R.A., MAYERS D.L., CHUNG R.C.Y., WAGNER K.F., KIM S.,
RA BIRX D.L., MICHAEL N.L.;
RT "Evolution of human immunodeficiency virus type 1 env sequence
variation in patients with diverse rates of disease progression and T-
cell function.";
RT J. Virol. 71:1871-1879(1996).
RL EMBL; U69437; AAC56748.1; -;
DR PFAM; PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1

FT NON_TER 244 244
SQ SEQUENCE 244 AA; 27027 MW; 11A44107 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 244;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVW 11
DB 71 SSVW 75

RESULT 10
P88358 ID P88358 PRELIMINARY; PRT; 251 AA.
AC P88358;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT H;
RX MEDLINE: 97184515.
RA MCDONALD R.A., MAYERS D.L., CHUNG R.C.Y., WAGNER K.F., KIM S.,
RA BIER D.L., MICHAEL N.L.;
RT "Evolution of human immunodeficiency virus type 1 env sequence
variation in patients with diverse rates of disease progression and T-
cell function."
RL J. Virol. 71:1871-1879(1996).
DR EMBL: U69434; AAC56745.1; -;
DR PFM: PF00516; GP120; 1.
KW Envelope protein.
FT NON_TER 1 1
FT NON_TER 251 251
SQ SEQUENCE 251 AA; 27714 MW; A06370E1 CRC32;

Query Match 35.7%; Score 5; DB 12; Length 251;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSVW 11
DB 78 SSVW 82

RESULT 11
Q22117 ID Q22117 PRELIMINARY; PRT; 255 AA.
AC Q22117;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE T03F7.5 PROTEIN.
GN T03F7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC MORTIMORE B.;
RA MORTIMORE B.;
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans."
RL Nature 368:32-38(1994).
DR EMBL: Z74041; CAA98520.1; -;
SQ SEQUENCE 255 AA; 29600 MW; FAC3B217 CRC32;

Query Match 35.7%; Score 5; DB 5; Length 255;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHW 6
DB 208 EFHW 212

RESULT 12
O10441 ID O10441 PRELIMINARY; PRT; 262 AA.
AC O10441;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE PUTATIVE 30 KDA PROTEIN.
GN L2 COMP. ORF.
OS Mouse adenovirus type 1 (MAY-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEISSNER J.D., HIRSCH G.N., LARUE E.A., FULCHER R.A., SPINDLER K.R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U95843; AAB53756.1; -;
SQ SEQUENCE 262 AA; 30266 MW; 6FE03EED CRC32;

Query Match 35.7%; Score 5; DB 12; Length 262;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RWSS 9
DB 59 RWSS 63

RESULT 13
O37972 ID O37972 PRELIMINARY; PRT; 263 AA.
AC O37972;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE INDOLETHYLAMINE N-METHYLTRANSFERASE.
GN INMT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE: 99069450.
RA THOMPSON M.A., WEINSHILBOUM R.M.;
RT "Rabbit lung indolethylamine N-methyltransferase. cDNA and gene
cloning and characterization."
RL J. Biol. Chem. 273:34502-34510(1998).
DR EMBL: AF077828; AAC97492.1; -;
DR EMBL: AF077827; AAC97492.1; JOINED.

DR EMBL; AF077826; AAC97491.1; --
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 263 AA; 28955 MW; CE43D9F6 CRC32;

Query Match 35.7%; Score 5; DB 6; Length 263;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSWYV 11
 Db 202 SSWYV 206
 |||||

RESULT 14
 Q52970 PRELIMINARY; PRT; 285 AA.
 AC Q52970;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE MODULATION GENES NODA, NODB AND NODC.
 OS Rhizobium meliloti.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85087953.
 RA TOEROEK I., KONDOROSI E., STEPKOWSKI T., POSFAI J., KONDOROSI A.;
 RT "Nucleotide sequence of Rhizobium meliloti nodulation genes.";
 RL Nucleic Acids Res. 12:9509-9524(1984).
 DR EMBL; X01649; CAA25807.1; --
 SQ SEQUENCE 285 AA; 32342 MW; 157B9F20 CRC32;

Query Match 35.7%; Score 5; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYN 10
 Db 86 WSSYN 90
 |||||

RESULT 15
 Q9XMG3 PRELIMINARY; PRT; 294 AA.
 AC Q9XMG3;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE ET2.OL ORF1 PROTEIN (FRAGMENT).
 GN ET2.OL ORF1.
 OS Epichloe typhina.
 OG Mitochondrion
 OG Mitochondrial plasmid.
 OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
 OC Hypocreales; Clavicipitaceae; Epichloe.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PRG; PLASMID-MITOCHONDRIAL PLASMID;
 RX MEDLINE; 92145777
 RA MOGEN K.L., SIEGEL M.R., SCHARDL C.L.;
 RT "Linear DNA plasmids of the perennial ryegrass choke pathogen,
 Epichloe typhina (Clavicipitaceae).";
 RL Curr. Genet. 20:519-526(1991).
 DR EMBL; X57200; CAA40486.2; --
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 294
 SQ SEQUENCE 294 AA; 35780 MW; 90A243F8 CRC32;

Query Match 35.7%; Score 5; DB 8; Length 294;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFHRW 6
 Db 197 EFHRW 201
 |||||

Search completed: September 13, 2000, 02:27:31
 Job time: 173 sec

US-09-155-076-1 x N90761 ..
Align seg 1/1 to: N90761 from: 1 to: 248

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||
11 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 52

seq_name: gb_est52:T28280

seq_documentation_block:
LOCUS T28280 254 bp mRNA EST 06-SEP-1995
DEFINITION EST35080 Human Embryo Homo sapiens cDNA 5' end similar to
acetylcholinesterase (HT:518), mRNA sequence.
ACCESSION T28280
VERSION T28280.1 GI:610378
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 254)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,A.R., Fuldner,R.A.,
Buit,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,J.P.S.,
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
JOURNAL Nature 377, 3-174 (1995)
MEDLINE 96026280
COMMENT On May 10, 1995 this sequence version replaced gi:805490.
Other ESTs: THC20776
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Insert Length: 1145 Std Error: 0.00
Seq primer: M13 Reverse
High quality sequence stop: 187.

BASE COUNT 45 a 89 c 78 g 41 t 1 others
ORIGIN

FEATURES
source

1..254
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="ATCC (inhost):101797"
/db_xref="taxon:9606"
/clone_lib="Human Embryo"
/tissue_type="embryo"
45 a 89 c 78 g 41 t 1 others

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x T28280 ..

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||
138 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 179

seq_name: gb_est25:AI764103

seq_documentation_block:
LOCUS AI764103 362 bp mRNA EST 25-JUN-1999
DEFINITION UI-R-Y0-acy-h-04-0-UI.s1 UI-R-Y0 Rattus norvegicus cDNA clone
UI-R-Y0-acy-h-04-0-UI 3', mRNA sequence.
ACCESSION AI764103
VERSION AI764103.1 GI:5210038
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 362)
AUTHORS Bonaldo,M.F., Lenon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
normalized Eye library cDNA Library Preparation: M.B. Soares Lab
Clone distribution: clones will be available through Research
Genetics (www.resgen.com) The following repetitive elements were
found in this cDNA sequence: 1-30, >POLY_A#simple_repeat
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source

1..362
Location/Qualifiers
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-Y0-acy-h-04-0-UI"
/clone_lib="UI-R-Y0"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A0, UI-R-A1, UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to

us-09-155-076-1.rst

Wed Sep 13 08:11:29 2000

double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996); TAG-LIB=UI-R-Y0; TAG-RISSUE=EYE; TAG_SEQ=CATTG"

BASE COUNT 71 a 87 c 116 g 88 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x A1764103/rev ..

Align seg 1/1 to reverse of: A1764103 from: 1 to: 362

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
340 GCCGAGTCCACCGCTGGAGCTCTACATGTCACACTGGAAG 299

seq_name: gb_est48:F27586

seq_documentation_block:
LOCUS F27586 378 bp mRNA EST 13-MAY-1999
DEFINITION HSPD15598 HM3 Homo sapiens cDNA clone s4000002G06, mRNA sequence.

ACCESSION F27586
VERSION F27586.1 GI:4813212
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 378)
AUTHORS Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfi, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
TITLE Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
JOURNAL Genome Res. 6 (1), 35-42 (1996)
MEDLINE 96276048
COMMENT On Jul 7, 1999 this sequence version replaced gi:5410190.

Contact: Valle G.
CRIBI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it.

FEATURES
Location/Qualifiers
1..378
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000002G06"
/clone_lib="HM3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNA11 (Invitrogen); Site.1: BstXI; Site.2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCGGCTCGAGCGCGCTTTTTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNA11 vector."

BASE COUNT 65 a 147 c 102 g 64 t

ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x F27586 ..

Align seg 1/1 to: F27586 from: 1 to: 378

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
115 GCCGAGTCCACCGCTGGAGCTCTACATGTCACACTGGAAG 156

seq_name: gb_est14:AA933814

seq_documentation_block:
LOCUS AA933814 380 bp mRNA EST 26-AUG-1998
DEFINITION O184009.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1536281 3', similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA933814
VERSION AA933814.1 GI:3090082
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 380)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Feb 11, 1998 this sequence version replaced gi:2873131.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CNDA Library Preparation: M. Bento Soares, Ph.D.
CNDA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 437 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1536281"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGATTCGCGCGCCGCAATATTTTATTTTATTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldi."

BASE COUNT 65 a 150 c 101 g 64 t

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AA933814

Align seg 1/1 to: AA933814 from: 1 to: 380

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

115 GCCGAGTTCACCGCTGAGCTCTACATGTCACACTGGAG 156

seq_name: gb_est44:AW612795

seq_documentation_block:

LOCUS AW612795 384 bp mRNA EST 23-MAR-2000
 DEFINITION hh33a07.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2956884 3'
 similar to contains PTR5.t3 PTR5 repetitive element ;, mRNA
 sequence.

ACCESSION

AW612795

VERSION

AW612795

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 384)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL

Tumor Gene Index

COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco.

FEATURES

source

1. 384

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2956884"

/clone_lib="NCI CGAP Lu24"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI CGAP Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (cloneIDs

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 154 c 96 g 68 t

ORIGIN

14

Quality: 14.00

Ratio: 1.000

Percent Similarity: 100.000

Percent Identity: 100.000

Gaps: 0

Length: 14

Alignment_block:

US-09-155-076-1 x AW612795

Align seg 1/1 to: AW612795 from: 1 to: 384

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
 88 GCCGAGTTCACCGCTGAGCTCTACATGTCACACTGGAG 129

seq_name: gb_est14:AA998511

seq_documentation_block:

LOCUS AA998511 393 bp mRNA EST 04-JUL-1999
 DEFINITION UI-R-CO-ie-h-11-0-UI-s1 UI-R-CO Rattus norvegicus cDNA clone
 UI-R-CO-ie-h-11-0-UI 3', mRNA sequence.

ACCESSION

AA998511

VERSION

AA998511.1

KEYWORDS

EST.

SOURCE

Rattus norvegicus

ORGANISM

Norway rat.

REFERENCE

1 (bases 1 to 393)

AUTHORS

Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE

Normalization and subtraction: two approaches to facilitate gene

JOURNAL

discovery

MEDLINE

97044477

COMMENT

On Jun 5, 1998 this sequence version replaced gi:3189162.

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9585

Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the

oligo-dr track served to identify it as a clone from the normalized

adult Brain library. cDNA Library Preparation: M. Fatima Bonaldo,

Ph.D. Clone distribution: clones will be available through Research

Genetics This clone is also available through the I.M.A.G.E.

Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1774140

Seq primer: M13 Forward

POLYA-No.

FEATURES

source

1. 393

Location/Qualifiers

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-CO-ie-h-11-0-UI"

/clone_lib="UI-R-CO"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CO

library is a subtracted library derived from the UI-R-Al

and UI-R-E1 libraries. The UI-R-Al library consisted of a

mixture of individually tagged normalized libraries

constructed from rat placenta, adult lung, brain, liver,

kidney, heart, spleen, ovary, and muscle. The UI-R-E1

library consisted of a mixture of individually tagged

normalized libraries constructed from 8, 12 and 18-day

embryo. The tag is a string of 3-5 nucleotides present

between the Not I site and the oligo-dr track which

allows identification of the library of origin of a clone

within the mixture. The subtracted library (UI-R-CO) was

constructed as follows: PCR amplified cDNA inserts from a

pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had

been derived was used as a driver in a hybridization with

the pooled UI-R-Al and UI-R-E1 library in the form of

single-stranded circles. The remaining single-stranded

circles (subtracted library) was purified by

hydroxyapatite column chromatography, converted to

double-stranded circles and electroporated into DH10B

bacteria (Life Technologies) to generate the UI-R-CO

library. This procedure has been previously described

(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,

Wed Sep 13 08:11:29 2000

BASE COUNT 80 a 92 c 130 g 91 t
 ORIGIN

alignment_scores:
 Quality: 14.00 Length: 14
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x AA998511/rev ..
 Align seg 1/1 to reverse of: AA998511 from: 1 to: 393

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 |||||
 327 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 286

seq_name: gb_est25:AI766812

seq_documentation_block: 395 bp mRNA 21-DEC-1999
 LOCUS AI766812
 DEFINITION w189a12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400478 3', similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI766812
 VERSION AI766812.1 GI:52333321

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 395)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Apr 7, 1998 this sequence version replaced gi:3034669.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA sequencing by: Greg Lennon, Ph.D.

Cloning distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 442 Std Error: 0.00

Seq primer: -40UP from Glibco.

Location/Qualifiers

1. .395

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2400478"

/clone_lib="NCI-CGAP_Kid12"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with

a modified polylinker; Site.1: Not I; Site.2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid5 was

prepared, and ss circles were made in vitro. Following RAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(cloneIDs 1323912-1325831, 1471368-1472903 and

1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo.

64 a 155 c 107 g 69 t

BASE COUNT

ORIGIN

alignment_scores:
 Quality: 14.00 Length: 14
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x AI766812 ..

Align seg 1/1 to: AI766812 from: 1 to: 395

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 |||||
 119 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 160

seq_name: gb_est26:AI847791

seq_documentation_block: 395 bp mRNA 15-JUL-1999
 LOCUS AI847791
 DEFINITION UI-M-AK1-aev-f-02-0-UI.s1 NIH_BMAP_MHY_N Mus musculus cDNA clone
 UI-M-AK1-aev-f-02-0-UI 3', mRNA sequence.

ACCESSION AI847791

VERSION AI847791.1 GI:5491697

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 395)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

On Apr 7, 1998 this sequence version replaced gi:3035605.

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: MEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NCI site
 and the oligo-dT track served to verify it as a clone from the
 normalized hypothalamus library cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
 available by the means that is soon to be determined. When NIH
 determines the means for distribution of the BMAP cDNA clones, this
 record will be updated accordingly when that means is determined.
 Seq primer: M13 Forward

FEATURES

source

Location/Qualifiers

1. .395

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-AK1-aev-f-02-0-UI"

/clone_lib="NIH_BMAP_MHY_N"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site.1: Not I; Site.2: Eco RI; The

NIH_BMAP_MHY_N library is a normalized library constructed

from mouse hypothalamus. The tag is a string of 5

nucleotides present between the Not I site and the

oligo-dT track. The library was constructed as described

by Bonaldo, Lennon and Soares, Genome Research 6:

791-806, 1996. Tissue provided by Ms. Annie Novakovich,

Zivic-Miller Laboratories.; TAG_LIB=NIH_BMAP_MHY_N;

TAG_TISSUE=hypothalamus; TAG_SEQ=CGGTA"

BASE COUNT 78 a 91 c 137 g 89 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AI847791/rev ..

Align seg 1/1 to reverse of: AI847791 from: 1 to: 395

1 AlaGluPheHisArgTTPSerSerTyrMetValHisTrpLys 14

|||||
329 GCCGAGTTCACCGCTGAGCTCTACATGGTCACCTGGAG 288

seq_name: gb_est19:AI360141

seq_documentation_block:

LOCUS AI360141 410 bp mRNA EST 16-FEB-1999
DEFINITION qy83d10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018611 3'
similar to gb:M55040 ACETYLCOLINESTERASE PRECURSOR
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI360141

VERSION AI360141.1 GI:4111762

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 410)

AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGA), Tumor Gene Index

Unpublished (1998)

On Jun 22, 1998 this sequence version replaced gi:3247207.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D. Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 440 Std Error: 0.00

Seq primer: -40UP from Gibco.

FEATURES

source

1..410
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2018611"

/clone_lib="NCI_CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH108"

/note="Organ: brain; Vector: pTT3D-Pac (Pharmacia) with a

modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTCAATCTCAAGTCGAGCGCGCATAGTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pTT3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

64 a 163 c 113 g 69 t 1 others

BASE COUNT

ORIGIN

alignment_scores:

Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AI360141 ..

Align seg 1/1 to: AI360141 from: 1 to: 410

1 AlaGluPheHisArgTTPSerSerTyrMetValHisTrpLys 14

|||||
119 GCCGAGTTCACCGCTGAGCTCTACATGGTCACCTGGAG 160

seq_name: gb_est24:AI690171

seq_documentation_block:

LOCUS AI690171 411 bp mRNA EST 16-DEC-1999
DEFINITION tx33a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271338 3'
similar to gb:M55040 ACETYLCOLINESTERASE PRECURSOR
(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI690171

VERSION AI690171.1 GI:4901465

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 411)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2286587.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 458 Std Error: 0.00

Seq primer: -40UP from Gibco.

FEATURES

source

1..411
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2271338"

/clone_lib="NCI_CGAP_Lu24"

/tissue_type="carcinoid"

/lab_host="DH108"

/note="Organ: lung; Vector: pTT3D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI_CGAP_Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (cloneIDs

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo."

66 a 162 c 113 g 70 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 |||||
 118 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCACTGGAAG 159

seq_name: gb_est45:AW653940

seq_documentation_block:
 LOCUS AW653940 496 bp mRNA EST 05-APR-2000
 DEFINITION 102878 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION AW653940
 VERSION AW653940.1 GI:7419766
 KEYWORDS EST.
 SOURCE Bos taurus.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 496)
 AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
 Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
 Keele,J.W.
 TITLE Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 JOURNAL Unpublished (2000)
 COMMENT Contact: Smith TPL
 USDA, ARS US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 112 row: B column: 5
 Seq primer: ATTTAGGTGACACTATAG.
 FEATURES
 source
 1..496
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 1BOV"
 /tissue_type="pooled"
 /lab_host="DH108"
 /note="Vector: PCMV SPORT6; Site:1: XbaI; Site:2: XhoI;
 Library made from pooled tissue from lymph node, ovary,
 fat, hypothalamus, and pituitary."
 BASE COUNT 91 a 177 c 137 g 91 t
 ORIGIN

alignment_scores:
 Quality: 14.00 Length: 14
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x AW653940 ..
 Align seg 1/1 to: AW653940 from: 1 to: 496

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 |||||
 186 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCACTGGAAG 227

seq_name: gb_est1:AA030863

seq_documentation_block:
 LOCUS AA030863 501 bp mRNA EST 21-AUG-1996
 DEFINITION mi45c07.r1 Soares mouse embryo NbMel13.5 14.5 Mus musculus cDNA
 clone IMAGE:466476 5' similar to gb:M55040 ACETYLCHOLINESTERASE

PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase (MOUSE); mRNA sequence.
 AA030863
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 501)
 REFERENCE
 AUTHORS
 Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:280292
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 168.

FEATURES

Source
 1..501
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:466476"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGGTACCAATCTGAGTGGAGCGCGCCGGAATTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 97 a 163 c 138 g 103 t
 ORIGIN

alignment_scores:
 Quality: 14.00 Length: 14
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x AA030863

Align seg 1/1 to: AA030863 from: 1 to: 501

1 AlaGluPheHisArgTrpSerSeryrMetValHisTrpLys 14
 |||||
 217 GCGGAGTCCACCGCTGGAGCTCTACATGTGTCAGTGGAG 258

seq_name: gb_est2:AA118440

seq_documentation_block:

LOCUS

DEFINITION

AA118440 514 bp mRNA EST 19-NOV-1996
 MO3407.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus
 cDNA clone IMAGE:555444 5', similar to gb:M55040
 ACETYLCHOLINESTERASE PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase (MOUSE); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 514)

REFERENCE

AUTHORS

Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE

JOURNAL

COMMENT

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:336236

Seq primer: -28M13 rev1 from Amersham

High quality sequence stop: 234.

FEATURES

Source

1..514

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:555444"

/clone_lib="Life Tech mouse embryo 13 5dpc 10666014"

/tissue_type="embryo"

/dev_stage="13.5dpc embryos"

/lab_host="DH10B"

/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site 1: Salt; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. 13.5dpc embryos. pCMV-SPORT2 vector."

BASE COUNT 89 a 180 c 130 g 115 t

ORIGIN

alignment_scores:

Quality: 14.00 Length: 14

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AA118440

Align seg 1/1 to: AA118440 from: 1 to: 514

1 AlaGluPheHisArgTrpSerSeryrMetValHisTrpLys 14

|||||

202 GCGGAGTCCACCGCTGGAGCTCTACATGTGTCAGTGGAG 243

us-09-155-076-1.rst

Wed Sep 13 08:11:29 2000

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:19:17 ; Search time 17.65 seconds
(without alignments)
18.788 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87
Sequence: 1 AEFHRWSSYVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	14	1 W35340	Human acetylcholin
2	87	100.0	39	1 R77010	Alternative human
3	87	100.0	45	1 W48800	C-terminal fragmen
4	87	100.0	45	1 W68144	Human AChE splice
5	87	100.0	45	1 W74586	Amino acid sequenc
6	87	100.0	500	1 R06990	Human foetal acety
7	87	100.0	613	1 R06989	Human acetylcholin
8	87	100.0	614	1 R80726	Human acetylcholin
9	80	92.0	575	1 W39078	Torpedo californic
10	80	92.0	575	1 W39079	Torpedo californic
11	62	71.3	602	1 R37442	Full-length human
12	62	71.3	635	1 P60097	Sequence of protei
13	62	71.3	635	1 R41509	Full-length foetal
14	40.5	46.6	510	1 R41195	Yeast delta 9 desa
15	40	46.0	124	1 R15441	Heavy chain variab
16	40	46.0	124	1 R54335	Anti-HIV gp120 imm
17	40	46.0	124	1 R54244	Anti-HIV gp120 imm
18	40	46.0	124	1 R54245	Anti-HIV gp120 imm
19	40	46.0	124	1 R54246	Anti-HIV gp120 imm
20	40	46.0	124	1 W01309	VH region of HIV n
21	40	46.0	124	1 W01309	VH region of HIV n
22	40	46.0	124	1 W01247	VH region of HIV n
23	40	46.0	124	1 W01227	VH region of HIV n
24	40	46.0	146	1 W01228	VH region of HIV n
25	39	44.8	124	1 R75617	VH Fab M556-13 bin
26	39	44.8	124	1 R75616	VH Fab M556-16 bin
27	39	44.8	124	1 R75615	VH Fab M556-15 bin
28	39	44.8	124	1 R75614	VH Fab M556-10 bin
29	39	44.8	124	1 R75613	VH Fab M556-7 bin
30	39	44.8	124	1 R75612	VH Fab M556-3 bind
31	39	44.8	124	1 R75611	VH Fab M556-2 bind
32	39	44.8	124	1 R75611	VH Fab M556-2 bind
33	39	44.8	124	1 R75611	VH Fab M556-2 bind

34 39 44.8 124 1 R75570
35 39 44.8 124 1 R75572
36 39 44.8 137 1 R62445
37 39 44.8 144 1 R08346
38 38 43.7 121 1 R28806
39 38 43.7 124 1 R54330
40 38 43.7 124 1 R54332
41 38 43.7 124 1 R54336
42 38 43.7 124 1 R54269
43 38 43.7 124 1 W01306
44 38 43.7 124 1 W01310
45 38 43.7 124 1 W01311

ALIGNMENTS

RESULT 1
W35340
ID W35340 standard; peptide; 14 AA.
AC W35340:
DT 17-APR-1998 (first entry)
DE Human acetylcholinesterase 14-mer peptide.
KW Acetylcholinesterase; AChE; neuronal degeneration;
KW Parkinson's disease; Alzheimer's disease; stroke; cancer;
KW calcium channel modulator; antibody; inhibitor.
OS Homo sapiens.
PN W09735962-A1.
PD 02-OCT-1997.
PF 21-MAR-1997; G00796.
PR 22-MAR-1996; GB-006040.
PI (ISIS-) ISIS INNOVATION LTD.
PI Greenfield SA, Vaux DJ;
DR WPI: 97-489626/45.
PT Peptide(s) from acetylcholine esterase which open calcium channels -
PT used for treating disorders of the central nervous system, cancer
PT and stroke
PS Claim 1; Page 20; 27pp; English.
CC This 14-mer peptide corresponds to residues 535-548 of the
CC Acetylcholinesterase mature protein. This peptide is known to
CC act alone or in synergism with a fragment of beta-amyloid to
CC contribute to neuronal degeneration. Compounds that inhibit the
CC biological activity of the novel peptides, and antibodies, can be
CC used to control cytoplasmic calcium ion currents in vivo, and are
CC useful for treating disorders of the central nervous system
CC (e.g. Parkinson's and Alzheimer's diseases), stroke and cancer.
SQ Sequence 14 AA;

Query Match 100.0% Score 87; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | | | | | | | |
DB 1 AEFHRWSSYVHWK 14

RESULT 2
R77010
ID R77010 standard; Protein; 39 AA.
AC R77010;
DT 31-MAR-1996. (first entry)
DE Alternative human acetylcholinesterase (AChE) protein.
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;
KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.
OS Homo sapiens.
PN W09523158-A1.
PD 31-AUG-1995.
PF 28-FEB-1995; U02806.
PR 28-FEB-1994; US-202755.
PR 09-JAN-1995; US-370156.
PA (KOHN/) KOHN K I.

gdb

PA (YISS) YISSUM RES & DEV CO.
 PI Shani M, Soreq H, Zakut H;
 DR WPI: 95-311499/40.
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -
 PT expressed in transgenic animal assay system for evaluating anti-ChE
 PT activity of organophosphate(s), etc. or as model of ChE imbalance
 PS Disclosure; Fig.6; 5pp; English.
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at
 CC neuromuscular junctions where it serves a vital function in
 CC modulating cholinergic neurotransmission. This alternatively
 CC spliced form of human AChE may be expressed in transgenic animals
 CC which are used in an assay system for determining the anti-ChE
 CC activity of organophosphates, carbamates, anti-ChE drugs, plant
 CC glycoalkaloids and snake venoms.
 SQ Sequence 39 AA;

Query Match 100.0%; Score 87; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
 |||||
 Db 11 AEFHRSSSYMVHWK 24

RESULT 3
 W48800
 ID W48800 standard; protein; 45 AA.
 AC W48800.
 DT 07-OCT-1998 (first entry)
 DE C-terminal fragment of human acetylcholine esterase variant E1-4.6.
 KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;
 KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;
 KW chemotherapeutic drug; central nervous system.
 OS Homo sapiens.

EH Key Location/Qualifiers
 FT Region 1..5
 FT /note= "This region is encoded by the 3' end of
 FT AChE exon 4"
 FT Region 6..45
 FT /note= "Residues encoded by AChE exon 6"
 FN WO9822132-A2.
 PD 28-MAY-1998.
 PE 20-NOV-1997; U21696.
 PR 21-JUL-1997; US-053200.
 PR 20-NOV-1996; US-031194.
 PR 12-DEC-1996; US-035266.
 PA (KOHN/) KOHN K I.
 PI (YISS) YISSUM RES & DEV CO.
 PI Friedman A, Kaufer D, Seidman S, Soreq H;
 DR WPI: 98-312172/27.
 FT Increasing the permeability of the blood/brain barrier - using e.g.
 FT adrenaline, atropine or acetylcholine esterase I4 splice variant
 FT peptide, useful for imaging and/or treatment of central nervous
 FT system disorders
 PS Disclosure; Fig 2; 71pp; English.
 CC The present sequence represents a C-terminal fragment of the human
 CC acetylcholine esterase splice variant E1-4.6. The AChE E1-4.6 variant
 CC comprises of residues encoded by exons 1-4 of AChE linked to residues
 CC encoded by the alternatively spliced AChE exon 6. The invention claims
 CC for the human acetylcholine esterase-I4 (AChE-I4) readthrough splice
 CC variant (W48797). The invention provides a pharmaceutical composition,
 CC for facilitating passage of compounds through the blood/brain barrier
 CC (BBB), comprising of AChE-I4, I4 peptide (see W48797) or AChE-I4
 CC analogues (such as the AChE E1-4.6 variant) together with a
 CC pharmaceutically acceptable carrier. The pharmaceutical composition
 CC is claimed to facilitate a reversible disruption of the BBB allowing
 CC transport of compounds through the BBB. The compounds, e.g. imaging
 CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful
 CC for the diagnosis and treatment of diseases or disorders of the CNS such
 CC as infections, neurochemical disorders, brain tumours, gliomas, etc.
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
 |||||
 Db 17 AEFHRSSSYMVHWK 30

RESULT 4
 W68144
 ID W68144 standard; protein; 45 AA.
 AC W68144;
 DT 05-OCT-1998 (first entry)
 DE Human AChE splice variant E1-4. 6.
 KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis;
 KW AChE; Parkinson's disease; Alzheimer's disease; central nervous system;
 KW neuromuscular junction; cholinergic signalling; brain.
 OS Homo sapiens.
 PN WO9826062-A2.
 PD 18-JUN-1998.
 PE 12-DEC-1997; U23598.
 PR 21-JUL-1997; US-053334.
 PR 12-DEC-1996; US-035266.
 PR 13-FEB-1997; US-037777.
 PR 02-MAY-1997; US-850347.
 PA (KOHN/) KOHN K I.
 PI (YISS) YISSUM RES & DEV CO.
 PI Eckstein F, Friedman A, Kaufer D, Seidman S, Soreq H;
 DR WPI: 98-348522/30.
 DT Synthetic nuclease resistant antisense oligodeoxynucleotides -
 DT directed against acetylcholinesterase, useful for treating
 PT Parkinson's and Alzheimer's diseases and myasthenia gravis
 PS Disclosure; Fig 12; 89pp; English.

CC This represents the amino acid sequence of a human acetylcholinesterase
 CC (AChE) splice variant. The invention provides sequences shown in V41278
 CC to V41285 that represent synthetic nuclease resistant antisense
 CC oligodeoxynucleotides which are capable of selectively modulating human
 CC acetylcholinesterase (AChE) production. These oligonucleotides are
 CC targeted to a splice junction in a splice variant of AChE mRNA and are
 CC capable of selectively modulating human AChE production in the central
 CC nervous system and neuromuscular junction. The invention also provides a
 CC method for determining the efficacy of these human AChE specific
 CC antisense oligonucleotides. These antisense oligonucleotides can be used
 CC to restore balanced cholinergic signalling in the brain, particularly
 CC related to learning and memory as well as stress disorders, Parkinson's
 CC and Alzheimer's disease. They can also be used to reduce production and
 CC therefore deposition of AChE in the neuromuscular junctions of patients
 CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low
 CC doses while avoiding many of the side effects associated with Tacrine and
 CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and
 CC related drugs for myasthenia gravis.
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
 |||||
 Db 17 AEFHRSSSYMVHWK 30

RESULT 5
 W74586
 ID W74586 standard; protein; 45 AA.
 AC W74586;
 DT 21-DEC-1998 (first entry)
 DE Amino acid sequence of the human AChE variant 1.
 KW Nuclease resistance; inhibition; human; acetyl-cholinesterase; AChE;

KW Central nervous system; CNS.
 OS Homo sapiens.
 PN WO9829486-A1.
 PD 11-SEP-1998.
 PF 06-MAR-1998; U04503.
 PR 06-MAR-1997; US-040203.
 PA (KOHN/) KOHN K I.
 PA (YISS) YISSUM RES & DEV CO.
 PI Seidman S, Shohami E, Soreq H;
 DR WPI; 98-506377/43.
 PT Treatment of injury to central nervous system - by administration of
 PT Inhibitor of acetylcholinesterase production
 PS Disclosure; Page 61; 88pp; English.
 CC This is the amino acid sequence of a human acetylcholinesterase
 CC (ACHE) variant used in the method of the invention, where inhibitors
 CC of ACHE are used to treat injury to the central nervous system (CNS).
 CC The ACHE inhibitor can also be used to facilitate transplantation of
 CC neuronal cells to the CNS of a patient. The inhibitor can also be
 CC used to improve hippocampal neuron survival following injury to the
 CC CNS. The CNS injuries that can be treated with the method include
 CC epilepsy, stroke, Huntington's disease, head injury, spinal injury,
 CC Pain, Parkinson's disease, myelin deficiencies, neuromuscular
 CC disorders, neurological pain, amyotrophic lateral sclerosis,
 CC Alzheimer's disease, and affective disorders of the brain.
 SQ Sequence 45 AA;

Query Match 100.0%; Score 87; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 17 AEFHRWSSYVHWK 30

RESULT 6
 R06990
 ID R06990 standard; protein; 500 AA.
 AC R06990;
 DT 16-JAN-1991 (first entry)
 DE Human foetal acetylcholinesterase (hACHE) primary transcript.
 KW Organophosphorous poisoning; OP; cancer; leukaemia;
 KW megakaryocytopoiesis; ovarian cancer.
 OS Homo sapiens.
 PN EP-388906-A.
 PD 26-SEP-1990.
 PR 20-MAR-1990; 105274.
 PR 21-MAR-1989; IL-089703.
 PA (YISS) YISSUM RES & DEV CO.
 PI Soreq H, Zakut H;
 DR WPI; 90-291865/39.
 DR N-PSDB; Q05999.
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
 PT cytopoietic disorders and ovarian carcinomas.
 PS Disclosure; Fig 1c; 47pp; English.
 CC Gene product is useful as an active pharmacological component for the
 CC prophylaxis and treatment of organophosphorous poisoning, and post-
 CC surgical apnea due to succinylcholine administration.
 CC cDNA probe to the sequence may be used in diagnosis of various
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.
 SQ Sequence 500 AA;

Query Match 100.0%; Score 87; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 472 AEFHRWSSYVHWK 485

RESULT 7
 R06989
 ID R06989 standard; protein; 613 AA.
 AC R06989;
 DT 16-JAN-1991 (first entry)
 DE Human acetylcholinesterase (hACHE) primary transcript.
 KW Organophosphorous poisoning; OP; cancer; leukaemia;
 KW megakaryocytopoiesis; ovarian cancer.
 OS Homo sapiens.
 PN EP-388906-A.
 PD 26-SEP-1990.
 PR 20-MAR-1990; 105274.
 PR 21-MAR-1989; IL-089703.
 PA (YISS) YISSUM RES & DEV CO.
 PI Soreq H, Zakut H;
 DR WPI; 90-291865/39.
 DR N-PSDB; Q05998.
 PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
 PT cytopoietic disorders and ovarian carcinomas.
 PS Claim 5; Page 25; 47pp; English.
 CC Gene product is useful as an active pharmacological component for the
 CC prophylaxis and treatment of organophosphorous poisoning, and post-
 CC surgical apnea due to succinylcholine administration.
 CC cDNA probe to the sequence may be used in diagnosis of various
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.
 SQ Sequence 613 AA;

Query Match 100.0%; Score 87; DB 1; Length 613;
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||||
 DB 585 AEFHRWSSYVHWK 598

RESULT 8
 R0726
 ID R0726 standard; protein; 614 AA.
 AC R0726;
 DT 31-MAR-1996 (first entry)
 DE Human acetylcholinesterase (ACHE) protein.
 KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;
 KW chromosome-7q22; acetylcholine-hydrolyzing enzyme.
 OS Homo sapiens.
 PN WO9523158-A1.
 PD 31-AUG-1995.
 PF 28-FEB-1995; U02806.
 PR 28-FEB-1994; US-202755.
 PR 09-JAN-1995; US-370156.
 PA (KOHN/) KOHN K I.
 PA (YISS) YISSUM RES & DEV CO.
 PI Shani M, Soreq H, Zakut H;
 DR WPI; 95-311499/40.
 DR N-PSDB; Q99002.
 PT Alternative forms of human acetyl cholinesterase (ChE) gene -
 PT expressed in transgenic animal assay system for evaluating anti-ChE
 PT activity of organo:phosphate(s), etc. or as model of ChE imbalance
 PS Claim 3; Fig.1B; 55pp; English.
 CC Human acetylcholinesterase (EC-3.1.1.7) is accumulated at
 CC neuromuscular junctions where it serves a vital function in
 CC modulating cholinergic neurotransmission. Alternatively spliced
 CC forms of human ACHE may be expressed in transgenic animals which
 CC are used in an assay system for determining the anti-ChE activity
 CC of organophosphates, carbamates, anti-ChE drugs, plant glycoalkaloids
 CC and snake venoms.
 SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 1; Length 614;

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Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
    | | | | | | | | | | | | | |
Db 586 AEFHRWSSYVHWK 599

RESULT 9
W39078
ID W39078 standard; protein; 575 AA.
AC W39078;
DE Torpedo californica acetylcholinesterase AChE.
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;
OS ray; chemical agent; treatment; prevention; aging; mutant.
OS Torpedo californica.
FH Key Location/Qualifiers
FT Region 67..94
FT Modified_site 59..61
FT Region 59..61
FT Modified_site 199
FT Region 199
FT Modified_site 254..265
FT Region 254..265
FT Modified_site 402..521
FT Region 402..521
FT Modified_site 416..418
FT Region 416..418
FT Modified_site 457..459
FT Region 457..459
FT Modified_site 533..535
FT Region 533..535
FT Modified_site 569..571
FT Region 569..571
FT Modified_site 575 AA.
PN US6695750-A.
PD 09-DEC-1997.
PF 25-NOV-1994; 348920.
PR 25-NOV-1994; US-348920.
PA (USSA ) US SEC OF ARMY.
PI Doctor BP, Maxwell D, Radic Z, Saxena A, Taylor P;
DR WPI; 98-041233/04.
PT Mutant Torpedo acetylcholinesterase - useful for detoxifying
PT organo-phosphate compounds
PS Claim 1; Fig 2; 12pp; English.
CC This sequence represents a variant of the enzyme acetylcholinesterase
CC (AChE) from Torpedo californica which is capable of detoxifying
CC organophosphates. This E199Q mutant has greater resistance to aging
CC than the wild-type AChE and can destroy organophosphates in an
CC environmentally friendly manner. When combined with an oxime, this
CC mutant's ability to detoxify several organophosphates is amplified
CC and is predicted to have applications for the detoxification of chemical
CC warfare agents such as sarin or as a means of treating or preventing the
CC deleterious effects of organophosphate exposure in organisms.
SQ Sequence 575 AA;

Query Match 92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred. No. 0.0002;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHWK 14
    | | | | | | | | | | | | | |
Db 548 EFRWSSYVHWK 560

RESULT 11
R37442
ID R37442 standard; protein; 602 AA.
AC R37442;
DE 06-OCT-1993 (first entry)
DE Full-length human pseudocholinesterase.
KW butylcholinesterase; acetylcholine acylhydrolase; EC3.1.1.8; psi-ChE;
KW pseudo-Ch; neurotransmitter; organophosphorus insecticide; OP-poison;
KW antidote.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..24
FT Modified_site 45..47
FT Modified_site 134..136
FT Modified_site 269..271
FT Modified_site 284..286
FT Modified_site 369..371
FT Modified_site 509..511
FT Modified_site 509..511

Query Match 92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred. No. 0.0002;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHWK 14
    | | | | | | | | | | | | | |
Db 548 EFRWSSYVHWK 560

RESULT 10
W39079
ID W39079 standard; protein; 575 AA.
AC W39079;
DE Torpedo californica acetylcholinesterase AChE mutant E199Q.
KW Acetylcholinesterase; AChE; organophosphate; detoxification; oxime;
OS ray; chemical agent; treatment; prevention; aging; mutant.
OS Torpedo californica.
FH Key Location/Qualifiers

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FT modified_site 514..516
 FT /note= "potential N-glycosylation site"
 FT active_site 226
 FT /note= "active site Serine"

US5215909-A.
 PD 01-JUN-1993.
 PF 18-JUN-1986; 875737.
 PR 21-AUG-1987; US-875737.
 PR 15-AUG-1990; US-572911.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Soreq H;
 DR WPI; 93-188509/23.
 DR N-PSDB; Q42496.
 PT Recombinant human gene encoding human pseudo-cholinesterase -
 PT used to treat organo-phosphorus poisoning
 PS Disclosure; Columns 35-40; 34pp; English.
 CC A cDNA library prepared from foetal brain mRNA was screened with
 CC degenerate probe pools based on the organophosphorus binding site of
 CC cholinesterases. A 764 nucleotide insert (designated FBChE12) was
 CC isolated from one positive clone and sequenced. This insert (Q42495),
 CC containing an ORF large enough to code for about half the subunit
 CC size of human cholinesterase, was used as a probe to obtain the full-
 CC length pseudo-cholinesterase sequence (Q42496).
 CC Sequence 602 AA;
 SQ

Query Match 71.3%; Score 62; DB 1; Length 602;
 Best Local Similarity 64.3%; Pred. No. 0.087;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 | | | | | : : : : :
 DB 573 AGFHRWNNYMDWK 586

RESULT 12

P60097
 ID P60097 standard; Protein; 635 AA.
 AC P60097;
 DT 27-JUN-1991 (first entry)
 DE Sequence of protein having human cholinesterase (ChE)
 DE activity.
 KW Organophosphorus poisoning; therapy; prophylaxis; diagnosis;
 KW pseudo-cholinesterase deficiency.
 OS Homo sapiens.
 PN EP-205200-A.
 PD 30-DEC-1986.
 PF 16-JUN-1986; 108189.
 PR 18-JUN-1985; IL-075553.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Soreq H;
 DR WPI; 86-340581/52.
 DR N-PSDB; N60111.
 PT Human cholinesterase-type proteins - produced by host cell contg.
 PT recombinant vector which contains DNA fragment coding for the
 PT enzyme
 PS Claim 17; Page 38-40; 44pp; English.
 CC Human cholinesterase-type proteins can be used for the prophylaxis
 CC or for the treatment of the effects of organophosphorus cpd.
 CC poisoning. Other uses include clinical detection of
 CC pseudo-cholinesterase deficiencies, elucidation of the active site
 CC topography and the AA sequence of AChE for the development of rapid
 CC simple clinical methods to detect poisoning or disease-related
 CC changes in ChEs, and for detecting mutations in ChE genes.
 CC Sequence 635 AA;
 SQ

Query Match 71.3%; Score 62; DB 1; Length 635;
 Best Local Similarity 64.3%; Pred. No. 0.092;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14

Db 606 AGFHRWNNYMDWK 619
 | | | | | : : : : :
 RESULT 13

R41509
 ID R41509 standard; Protein; 635 AA.
 AC R41509;
 DT 06-OCT-1993 (first entry)
 DE Full-length foetal human pseudo-cholinesterase.
 DE butyrylcholinesterase; acetylcholine acylhydrolase; EC3.1.1.8; psi-ChE;
 KW pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;
 KW antidote.
 OS Homo sapiens.
 DR WPI; 93-188509/23.
 DR N-PSDB; Q42496.
 FT Key
 FT Location/Qualifiers
 FT peptide 35..58
 FT /note= "putative leader peptide"
 FT modified_site 79..81
 FT /note= "potential N-glycosylation site"
 FT modified_site 168..170
 FT /note= "potential N-glycosylation site"
 FT modified_site 303..305
 FT /note= "potential N-glycosylation site"
 FT modified_site 318..320
 FT /note= "potential N-glycosylation site"
 FT modified_site 403..405
 FT /note= "potential N-glycosylation site"
 FT modified_site 506..508
 FT /note= "potential N-glycosylation site"
 FT modified_site 543..545
 FT /note= "potential N-glycosylation site"
 FT active_site 260
 FT /note= "active site serine"
 FT US5215909-A.
 PN 01-JUN-1993.
 PD 18-JUN-1986; 875737.
 PR 18-JUN-1986; US-875737.
 PR 21-AUG-1987; US-087724.
 PR 15-AUG-1990; US-572911.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Soreq H;
 DR WPI; 93-188509/23.
 DR N-PSDB; Q48393.
 PT Recombinant human gene encoding human pseudo-cholinesterase -
 PT used to treat organo-phosphorus poisoning
 PS Claim 4; Columns 41-46; 34pp; English.
 CC A cDNA library prepared from foetal brain mRNA was screened with
 CC degenerate probe pools based on the organophosphorus binding site of
 CC cholinesterases. A 764 nucleotide insert (designated FBChE12) was
 CC isolated from one positive clone and sequenced. This insert (Q42495),
 CC containing an ORF large enough to code for about half the subunit
 CC size of human cholinesterase, was used as a probe to obtain the full-
 CC length pseudo-cholinesterase sequence by screening a foetal liver
 CC cDNA library and a primary glioblastoma cDNA library (Q48393).
 CC This sequence differs from sequence Q42496, particularly in the
 CC 3'-UTR.
 CC Sequence 635 AA;
 SQ

Query Match 71.3%; Score 62; DB 1; Length 635;
 Best Local Similarity 64.3%; Pred. No. 0.092;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 | | | | | : : : : :
 DB 606 AGFHRWNNYMDWK 619

RESULT 14

R41195
 ID R41195 standard; Protein; 510 AA.
 AC R41195;
 DT 18-MAR-1994 (first entry)

DE Yeast delta 9 desaturase gene.
 KW Delta-9 desaturase; fatty acids; seed oil; Zea maize;
 KW Brassica rapa; Brassica napus; yeast; crops; ss.
 OS Saccharomyces cerevisiae.
 PN EP-561569-A.
 PD 22-SEP-1993.
 PF 12-MAR-1993; 301895.
 PR 13-MAR-1992; US-850714.
 PA (JUBR) LOBRIZOL CORP.
 PI Mehra-palta A, Poutre CG;
 DR WPI; 93-296843/38.
 DR N-PSDB; Q48731.
 PT Plant seed contg. yeast delta-9 desaturase gene - used to produce
 oil with lower proportion of saturated fatty acids
 PS Disclosure; Page 21-22; 32pp; English.
 CC The yeast delta-9 desaturase gene was placed under the control of a
 phaseolin promoter (normal or truncated) or 35S promoter to drive
 expression in plant seeds transformed with the gene. Plant seeds
 preferably used are Zea maize (a monocot plant) and Brassica rapa or
 Brassica napus (dicots). Expression of the yeast delta-9 saturase
 gene in any plant seed tissue could result in a decrease in
 saturated fatty acids and an increase in monounsaturated fatty acids
 in the seed oil.
 SQ Sequence 510 AA;

Query Match 46.6%; Score 40.5; DB 1; Length 510;
 Best Local Similarity 56.2%; Pred. No. 99;
 Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 2;

QY 1 AEFHR-WS--SYMVHW 13
 :||| ||||
 DB 158 AGYHRLWSHRSYSAHW 173

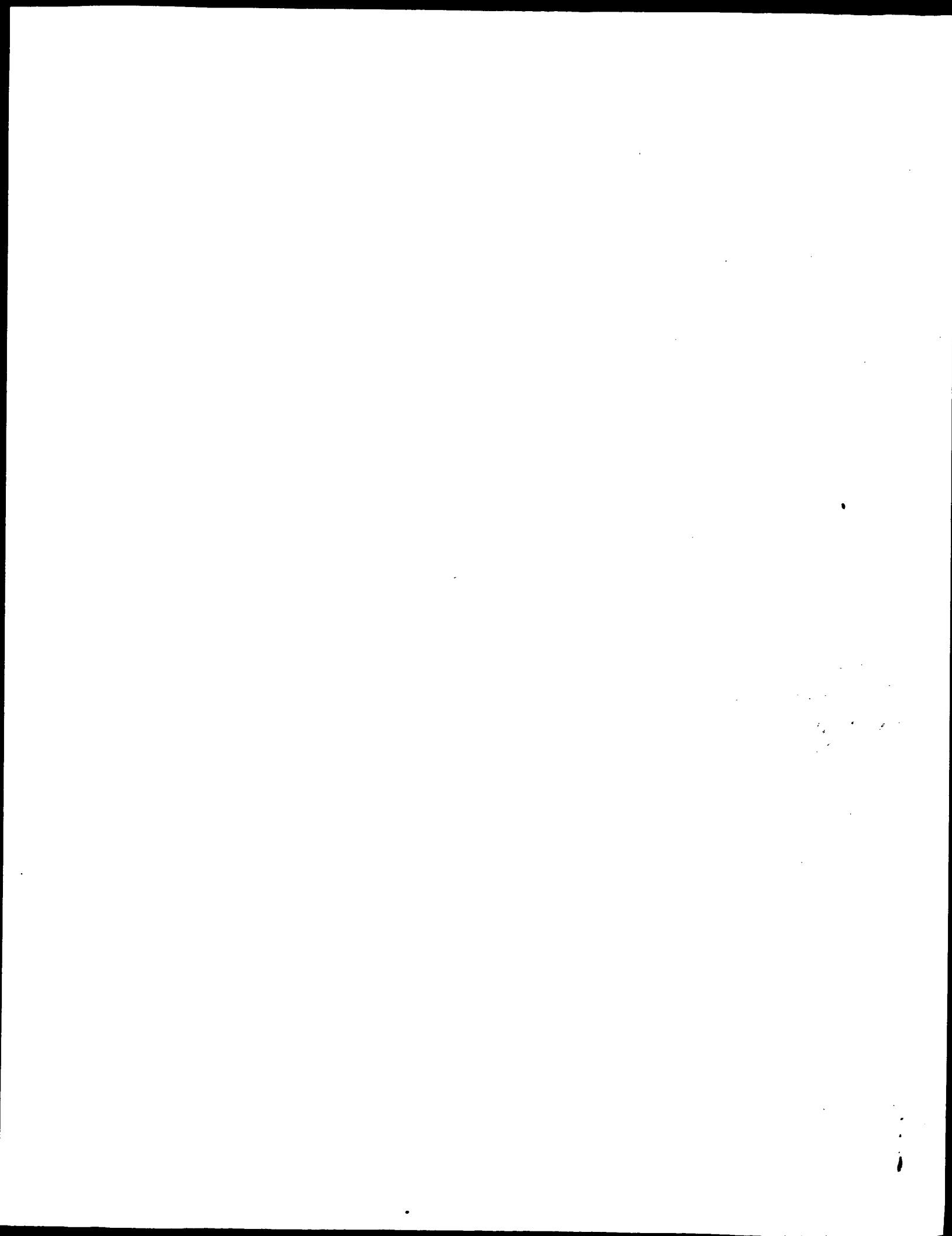
RESULT 15
 R15441
 ID R15441 standard; Protein; 124 AA.
 AC R15441;
 DT 25-FEB-1992 (first entry)
 DE Heavy chain variable region of MAb 18B9.
 KW HRV; ICAM-1; antigen-binding fragment; inflammation;
 KW auto-immune disease.
 OS Homo sapiens.
 PN EP-459577-A.
 PD 04-DEC-1991.
 PF 25-MAY-1991; 201243.
 PR 01-JUN-1990; US-532001.
 PA (MERI) MERCK & CO INC.
 PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
 DR WPI; 91-355850/49.
 PT Microbially expressed portions of monoclonal antibody - can block
 PT attachment of rhinovirus ligands to inter-cellular adhesion
 PT molecule (ICAM-1)
 PS Claim 1; Page 20; 28pp; English.
 CC This is one of six antibody fragments from MAb's specific for domain
 1 of ICAM-1. The peptide fragments can be used to treat or prevent
 CC rhinovirus infection. See R15437-R15443.
 SQ Sequence 124 AA;

Query Match 46.0%; Score 40; DB 1; Length 124;
 Best Local Similarity 38.5%; Pred. No. 27;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHW 13
 | | :|:|
 DB 24 ASGHFTSFVIHW 36

us-09-155-076-l_1.rag

Wed Sep 13 08:11:29 2000



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:19:42 ; Search time 14.59 Seconds
(without alignments)
14.709 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSYMHVK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 152396 seqs, 15329161 residues
Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PCRUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	87	100.0	40	2	US-08-370-156-25
2	87	100.0	45	2	US-08-370-156-7
3	87	100.0	45	2	US-08-370-156-8
4	87	100.0	614	1	US-07-732-962A-2
5	87	100.0	614	2	US-08-370-156-2
6	87	100.0	614	3	US-08-446-100-19
7	87	100.0	614	3	US-08-446-100-20
8	87	100.0	614	3	US-08-446-100-21
9	87	100.0	614	3	US-08-446-100-22
10	87	100.0	614	3	US-08-446-100-23
11	87	100.0	614	3	US-08-446-100-25
12	87	100.0	614	3	US-08-814-095-2
13	87	100.0	614	3	PCT-US92-08106-2
14	80	92.0	575	1	US-08-348-920-1
15	80	92.0	575	1	US-08-348-920-2
16	62	71.3	572	5	5200183-5
17	62	71.3	573	5	5215909-12
18	62	71.3	602	3	US-08-446-100-1
19	62	71.3	602	3	US-08-446-100-2
20	62	71.3	602	3	US-08-446-100-3
21	62	71.3	602	3	US-08-446-100-4
22	62	71.3	602	3	US-08-446-100-5
23	62	71.3	602	3	US-08-446-100-6
24	62	71.3	602	3	US-08-446-100-7
25	62	71.3	602	3	US-08-446-100-8
26	62	71.3	602	3	US-08-446-100-9
27	62	71.3	602	3	US-08-446-100-10
28	62	71.3	602	3	US-08-446-100-11

29 71.3 602 3 US-08-446-100-12 Sequence 12, Appl
30 71.3 602 3 US-08-446-100-13 Sequence 13, Appl
31 71.3 602 3 US-08-446-100-14 Sequence 14, Appl
32 71.3 602 3 US-08-446-100-15 Sequence 15, Appl
33 71.3 602 3 US-08-446-100-16 Sequence 16, Appl
34 71.3 602 3 US-08-446-100-17 Sequence 17, Appl
35 71.3 602 3 US-08-446-100-18 Sequence 18, Appl
36 71.3 602 3 US-08-446-100-19 Sequence 19, Appl
37 71.3 602 3 US-08-446-100-20 Sequence 20, Appl
38 71.3 602 3 US-08-446-100-21 Sequence 21, Appl
39 71.3 602 3 US-08-446-100-22 Sequence 22, Appl
40 71.3 602 3 US-08-446-100-23 Sequence 23, Appl
41 71.3 602 3 US-08-446-100-24 Sequence 24, Appl
42 71.3 602 3 US-08-446-100-25 Sequence 25, Appl
43 71.3 602 3 US-08-446-100-26 Sequence 26, Appl
44 71.3 602 3 US-08-446-100-27 Sequence 27, Appl
45 71.3 602 3 US-08-446-100-28 Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-370-156-25
; Sequence 25, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mullford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-156-25

Query Match 100.0%; Score 87; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : 1 AEFHRWSSYMHVK 14

DB : 12 AEFHRWSSYMHVK 25

RESULT 2
US-08-370-156-7
; Sequence 7, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-156-7

Query Match 100.0%; Score 87; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMVHWK 14
| | | | | | | | | | | | | | | |
Db 17 AEFHRSSSYMVHWK 30

RESULT 3
US-08-370-156-8
; Sequence 8, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-156-8

Query Match 100.0%; Score 87; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRSSSYMVHWK 14
| | | | | | | | | | | | | | | |
Db 17 AEFHRSSSYMVHWK 30

RESULT 4
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-732-962A-2

Query Match 100.0%; Score 87; DB 1; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 586 AEFHRWSSYVHWK 599

RESULT 5

US-08-370-156-2
 ; Sequence 2, Application US/08370156
 ; Patent No. 5932780
 ; GENERAL INFORMATION:
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Zakut, Haim
 ; APPLICANT: Shani, Moshe
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 ; ANTICHOLINESTERASE SUBSTANCES
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reising, Ethlington, Barnard & Perry
 ; STREET: P.O. Box 4390
 ; CITY: Troy
 ; STATE: Michigan
 ; COUNTRY: US
 ; ZIP: 48099
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/370,156
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kohn, Kenneth I.
 ; REGISTRATION NUMBER: 30,955
 ; REFERENCE/DOCKET NUMBER: P-307 (Mullford)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (810) 689-3500
 ; TELEFAX: (810) 689-4071
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 614 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-370-156-2

Query Match 100.0%; Score 87; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 586 AEFHRWSSYVHWK 599

RESULT 6

US-08-446-100-19
 ; Sequence 19, Application US/08446100
 ; Patent No. 6001625
 ; GENERAL INFORMATION:
 ; APPLICANT: Broomfield, Clarence A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Lockridge, Oksana
 ; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Hendricks and Assoc.
 STREET: 9669 A Main Street, P.O. Box 2509
 CITY: Fairfax
 STATE: VA
 COUNTRY: US
 ZIP: 22031
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,100
 ; FILING DATE: 19-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hendricks, Glenna
 ; REGISTRATION NUMBER: 32,535
 ; REFERENCE/DOCKET NUMBER: Broomfield
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 425-4250
 ; TELEFAX: (703) 425-2767
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 614 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: human esterases
 ; US-08-446-100-19

Query Match 100.0%; Score 87; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14
 Db 586 AEFHRWSSYVHWK 599

RESULT 7

US-08-446-100-20
 ; Sequence 20, Application US/08446100
 ; Patent No. 6001625
 ; GENERAL INFORMATION:
 ; APPLICANT: Broomfield, Clarence A
 ; APPLICANT: Millard, Charles B
 ; APPLICANT: Lockridge, Oksana
 ; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hendricks and Assoc.
 ; STREET: 9669 A Main Street, P.O. Box 2509
 ; CITY: Fairfax
 ; STATE: VA
 ; COUNTRY: US
 ; ZIP: 22031
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,100
 ; FILING DATE: 19-MAY-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

```
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-20

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 8
US-08-446-100-21
; Sequence 21, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
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; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-21

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 9
US-08-446-100-22
; Sequence 22, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-22

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
Db 586 AEFHRWSSYVHWK 599

RESULT 10
US-08-446-100-23
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; Sequence 23, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-23

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
|||
Db 586 AEFHRWSSYMVHWK 599

RESULT 11
US-08-446-100-25
; Sequence 25, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-25

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Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
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Db 586 AEFHRWSSYMVHWK 599

RESULT 12
US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814.095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 614 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-814-095-2

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 586 AEFHRWSSYVHWK 599

RESULT 13

PCT-US92-06106-2

Sequence 2, Application PC/TUS9206106

GENERAL INFORMATION:

APPLICANT: Fischer, Melir

TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN

TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White, Esq.

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06106

FILING DATE: 19920722

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-06106-2

Query Match

Best Local Similarity 100.0%; Score 87; DB 4; Length 614;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
|||||
DB 586 AEFHRWSSYVHWK 599

RESULT 14

US-08-348-920-1

Sequence 1, Application US/08348920
Patent No. 5695750

GENERAL INFORMATION:

APPLICANT: Doctor, Bhupendra P.

APPLICANT: Maxwell, Donald

APPLICANT: Saxena, Ashima

APPLICANT: Radic, Zoran

APPLICANT: Taylor, Palmer

TITLE OF INVENTION: Compositions for Use to Deactivate

TITLE OF INVENTION: Organophosphates

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: John F. Moran

STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort

STREET: Detrick

CITY: Frederick

STATE: MD

COUNTRY: US

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/348,920

FILING DATE: 25-NOV-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna

REGISTRATION NUMBER: 32,535

REFERENCE/DOCKET NUMBER: doc348,920

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-7807

TELEFAX: 301-619-7714

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 575 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-08-348-920-1

Query Match 92.0%; Score 80; DB 1; Length 575;

Best Local Similarity 92.3%; Pred. No. 0.00054;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 548 EFRWSSYVHWK 560

RESULT 15

US-08-348-920-2

Sequence 2, Application US/08348920

Patent No. 5695750

GENERAL INFORMATION:

APPLICANT: Doctor, Bhupendra P.

APPLICANT: Maxwell, Donald

APPLICANT: Saxena, Ashima

APPLICANT: Radic, Zoran

APPLICANT: Taylor, Palmer

TITLE OF INVENTION: Compositions for Use to Deactivate

TITLE OF INVENTION: Organophosphates

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: John F. Moran

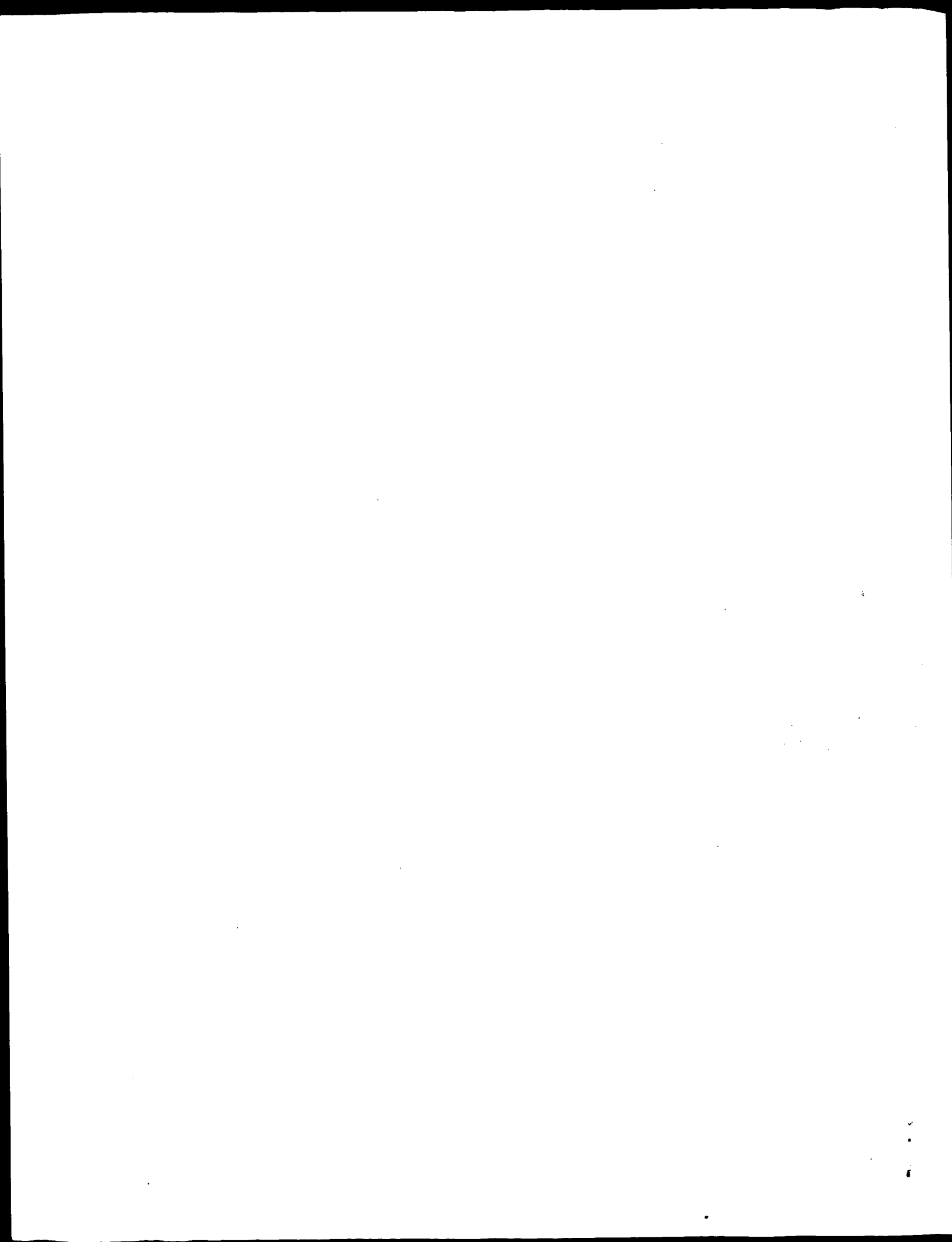
STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort

STREET: Detrick
CITY: Frederick
STATE: MD
COUNTRY: US
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,920
FILING DATE: 25-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: doc348,920
TELEPHONE: (301) 619-7807
TELEFAX: 301-619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-348-920-2

Query Match 92.0%; Score 80; DB 1; Length 575;
Best Local Similarity 92.3%; Pred.No. 0.00054;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 548 EFHRWSSYMHVK 560

Search completed: September 13, 2000, 02:22:01
Job time: 139 sec



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 Date: Sep 13, 2000 2:56 AM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

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Search information block:

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 Query length: 14
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 Database sequences: 972840
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gb_om:OCU05036	87.00	238.77	3.3e-05	1947	U05036 Oryctolagus cuniculus a
gb_ro:SM0879	87.00	238.22	3.5e-05	2066	S0879 acetylcholinesterase T
gb_ro:SM0879	87.00	238.22	3.5e-05	2069	X5618 Mouse mRNA for acetylch
gb_pr2:HUMACHE	87.00	237.61	3.8e-05	2218	M5504 Human acetylcholinester
gb_pr2:HUMACHE	87.00	237.61	3.8e-05	2256	AR070205 Sequence 5 from paten
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gb_pr2:HUMACHE	87.00	173.32	0.1475	1878	U03472 Gallus gallus acetylch
gb_pr2:HUMACHE	87.00	166.37	0.3598	4536	M32391 Human butyrylcholineste
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gb_pr2:HUMACHE	87.00	165.16	0.4202	1696	AF178685 Equus caballus butyry
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gb_pr2:HUMACHE	87.00	162.28	0.6082	2445	E01187 DNA encoding human ChE
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gb_pr2:HUMACHE	87.00	107.57	678.12	57085	AC017905 Drosophila melanog
gb_pr2:HUMACHE	87.00	95.08	3.4e+03	278748	AE003535 Drosophila melanog

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 gb_h4:AC006734 - 51.00 96.83 2.7e+03 152637 ! AC006734 Caenorhabditis e
 gb_h4:AC012308 - 51.00 96.11 2.9e+03 167300 ! AC012308 Homo sapiens clo
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seq_name: gb_om:BTACHE4

seq documentation block:

LOCUS BTACHE4 140 bp DNA 16-OCT-1998
 DEFINITION Bos taurus acetylcholinesterase T-subunit precursor (AChE) gene,
 exon 6 and partial cds.

ACCESSION AF061816

VERSION AF061816.1 GI:3746574

KEYWORDS 4 of 4

SEGMENT Bos taurus.

SOURCE Bos taurus.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae;

REFERENCE 1 (bases 1 to 140)

Mendelson, I., Kroman, C., Ariel, N., Shafferman, A. and Velan, B.

Characterization

Biochem. J. 334 (Pt 1), 251-259 (1998)

JOURNAL MEDLINE

REFERENCE 2 (bases 1 to 140)

Mendelson, I., Kroman, C., Ariel, N., Shafferman, A. and Velan, B.

Direct Submission

Submitted (28-APR-1998) Biochemistry and Molecular Genetics, Israel

Institute for Biological Research, PO Box 19, Ness Ziona 70450,

Israel

FEATURES

Location/Qualifiers

1..140

/organism="Bos taurus"

/db_xref="taxon:9913"

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/sex="male"

/tissue-type="kidney"

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/function="cholinesterase"

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BASE COUNT 32 a 39 c 47 g 22 t

ORIGIN

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Quality: 87.00 Length: 14
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 Percent similarity: 100.000 Percent identity: 100.000

alignment_block:

US-09-155-076-1 x BTACHE4

Align, seg 1/1 to: BTACHE4 from: 1 to: 140

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LOCUS HUMACHE04 475 bp DNA PRI 14-JUN-1995
DEFINITION Human acetylcholinesterase (ACHE) gene, exon 6.
ACCESSION L22562
VERSION L22562.1 GI:862302
KEYWORDS acetylcholinesterase.
SEGMENT 4 of 4
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,
Neville,L., Lieman-Hurwitz,J., Lev-Lehman,E., Ginzberg,D.,
Lapidot-Lifson,Y. and Zakut,H.
TITLE Molecular cloning and construction of the coding region for human
acetylcholinesterase reveals a G + C-rich attenuating structure
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)
JOURNAL 91088577
MEDLINE
REFERENCE 2 (sites)
AUTHORS Li,Y., Camp,S., Rachinsky,T.L., Getman,D. and Taylor,P.
TITLE Gene structure of mammalian acetylcholinesterase. Alternative exons
dictate tissue-specific expression
J. Biol. Chem. 266 (34), 23083-23090 (1991)
JOURNAL 92078174
MEDLINE
REFERENCE 3 (bases 1 to 475)
AUTHORS Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for VT blood group polymorphism
Am. J. Hum. Genet. 52 (5), 928-936 (1993)
JOURNAL 93256075
MEDLINE
COMMENT On Jun 15, 1995 this sequence version replaced gi:857448.
**Reference [1] reports bases 142-480;
Reference [J. Biol. Chem. 266, 23083-23090 (1991)] reports bases
132-141;
Reference [3] reports bases 1-131**.
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Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x HUMACHE04 ..

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DEFINITION Oryctolagus cuniculus acetylcholinesterase mRNA, partial cds.
ACCESSION U05036
VERSION U05036.1 GI:576446
KEYWORDS
SOURCE Oryctolagus cuniculus.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1947)
AUTHORS Jbilo,O., Lhermite,Y., Toutant,J. and Chatonnet,A.
TITLE Acetylcholinesterase and butyrylcholinesterase expression in adult
rabbit tissues and during development
Eur. J. Biochem. 225, 115-124 (1994)
JOURNAL 95010036
MEDLINE
REFERENCE 2 (bases 1 to 1947)
AUTHORS Chatonnet,A.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1994) Arnaud Chatonnet, Physiologie Animale,
Institut National de la Recherche Agronomique, Place Viala,
Montpellier, 34060 France
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/db_xref="taxon:9986"
/clone="epiph"
/tissue_type="muscle"
/dev_stage="adult"
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/EC_number="3.1.1.7"
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QQYVSLNLRPLEVRGLRAQACAFWNRLFKLLSATDTLDEAEKQWAEFHRSSYAV
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polyA_site 1946
BASE COUNT 299 a 655 c 660 g 333 t
ORIGIN

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alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x OCU05036 ..

Align seg 1/1 to: OCU05036 from: 1 to: 1947

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1 AlaGlupHeHisArgTrpSerSerTyrMetValHisTrpLys 14
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seq_name: gb_ro:S50879

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seq_documentation_block:
LOCUS S50879 2066 bp mRNA ROD 08-MAY-1993
DEFINITION acetylcholinesterase T subunit [rats, mRNA Partial, 2066 nt].

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TITLE Molecular cloning and construction of the coding region for human acetylcholinesterase reveals a G + C-rich attenuating structure
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)
MEDLINE 91088577
FEATURES

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Location/Qualifiers
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/dev_stage="21-week-old fetus"
/tissue_lib="lambda-gt10"
/map="7q22"
1..2218
/gene="ACHE"
/note="G00-118-746"
/product="acetylcholinesterase"
1..2218
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157..2001
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/EC_number="3.1.1.7"
/codon_start=1
/db_xref="GDB:G00-118-746"
/product="acetylcholinesterase"
/protein_id="AAA68151.1"
/db_xref="GI:177975"
/translation="MRPQCLHTPSPASPLLLLLWLGSGVGAEGREDAELLVTVR
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LDVYDGRFLVQARTVLSVMNRYVGFALPGSREAPNGVLLDQRLALQWQENV
AAGGDPSTSVLFESAGASVGMHLLSPFSGRLFRVAVLQSGAPNGPWATVGMGEAR
RATQALHLVCGPGGTGNDTELVAQLTRPAQVLNVHEWHLVPOESVFRFSFVPPV
DGLSDTFEALINAGDFHGLQVLGVVKGDEGSYFLVYGAPFSKONESLISRAEFLA
GYRVGYPQVSLAEANVLYHTDMLHPEDPARLEALSDVVDHNVVCPVAQLAGRLA
AGQARVAYFEHRASTLWPMGVPHGHEIEFIFGIPIDPSRNTAEKIKFAQRLM
RYWANFATPEPRDPKAPQPPYTAGAQQVVSQDLRLPLEVRRLQAQAFWNRFL
LPKLLSATDTLDEAEQWKAEFHRWSSYMHWNKQFDHYSKQDRCSDL"
229..291
/gene="ACHE"
/note="G00-118-746; does not fit consensus"
310..1998
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/note="G00-118-746"
/product="acetylcholinesterase"
BASE COUNT 355 a 755 c 580 g 428 t
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Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: HUMACHE from: 1 to: 2218
1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1912 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 1953
seq_name: gb_pat:AR070205
seq_documentation_block:
LOCUS AR070205 2256 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5891725.
ACCESSION AR070205
VERSION AR070205.1 GI:7221093
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x HUMACHE ..
Align seg 1/1 to: HUMACHE from: 1 to: 2218
1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1912 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 1953
seq_name: gb_pat:AR070205
seq_documentation_block:
LOCUS AR070205 2256 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5891725.
ACCESSION AR070205
VERSION AR070205.1 GI:7221093
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2256)
AUTHORS Soreq, H., Zakut, H. and Eckstein, F.
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them
JOURNAL Patent: US 5891725-A 5 06-APR-1999;
FEATURES Location/Qualifiers
source 1..2256
BASE COUNT 390 a 757 c 680 g 429 t
ORIGIN
alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x AR070205 ..
Align seg 1/1 to: AR070205 from: 1 to: 2256
1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1915 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 1956
seq_name: gb_pat:AR070207
seq_documentation_block:
LOCUS AR070207 3016 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 7 from patent US 5891725.
ACCESSION AR070207
VERSION AR070207.1 GI:7221095
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3016)
AUTHORS Soreq, H., Zakut, H. and Eckstein, F.
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical compositions containing them
JOURNAL Patent: US 5891725-A 7 06-APR-1999;
FEATURES Location/Qualifiers
source 1..3016
BASE COUNT 497 a 1065 c 840 g 614 t
ORIGIN
alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x AR070207 ..
Align seg 1/1 to: AR070207 from: 1 to: 3016
1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
2675 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 2716
seq_name: gb_pat:AR070206
seq_documentation_block:
LOCUS AR070206 3096 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5891725.
ACCESSION AR070206
VERSION AR070206.1 GI:7221094
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x AR070207 ..
Align seg 1/1 to: AR070207 from: 1 to: 3016
1 AlaCluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
2675 GCCGAGTTCACCGCTGGAGCTCTACATGCTGCTGCTGGAAG 2716
seq_name: gb_pat:AR070206
seq_documentation_block:
LOCUS AR070206 3096 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5891725.
ACCESSION AR070206
VERSION AR070206.1 GI:7221094
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.


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Unclassified.
REFERENCE 1 (bases 1 to 3096)
AUTHORS Sorreg,H., Zakut,H. and Eckstein,F.
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical
compositions containing them
JOURNAL Patent: US 5891725-A 6 06-APR-1999;
FEATURES Location/Qualifiers
source 1..3096
/organism="unknown"
BASE COUNT 509 a 1089 c 872 g 626 t
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AR070206 ..
Align seg 1/1 to: AR070206 from: 1 to: 3096

1 AlaGluPheHisArgTyrSerMetValHisTrpLys 14
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2755 GCCAGATCCACCGCTGCAGCTCTACATGCTGCACGTGGAAG 2796

seq_name: gb_om:AF053485

seq_documentation_block:
LOCUS AF053485 3958 bp DNA MAM 01-APR-1998
DEFINITION Felis catus acetylcholinesterase glycopospholipid-anchored form
precursor (ACHE) and acetylcholinesterase collagen-tailed or
globular form precursor (ACHE) genes, complete cds.
ACCESSION AF053485
VERSION AF053485.1 GI:3003019
KEYWORDS cat.
SOURCE Felis catus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE 1 (bases 1 to 3958)
AUTHORS Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE Sequence and characterization of domestic cat acetylcholinesterase
and butyrylcholinesterase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3958)
AUTHORS Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-1998) Eppley Institute, University of Nebraska
Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA
FEATURES
source 1..3958
/organism="Felis catus"
/db_xref="taxon:9685"
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/gene="ACHE"
/product="acetylcholinesterase collagen-tailed or globular
form precursor"
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/product="acetylcholinesterase glycopospholipid-anchored
form precursor"
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/codon_start=1
/product="acetylcholinesterase glycopospholipid-anchored
form precursor"
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/db_xref="GI:3003021"

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YDGRFLAQAGTIVLSMYRVGAFGLALPGSREAPGVNGLDQRLALQWQDNVATF
GGDPMSTVLFSGSAGASVGMHLLSPFSGRLGFLHRAVLQSGAPNGVATVGVGEARRA
TLLARLVGCPGGAGNDTELVAQLTRPAQDLVDHEWHVLPQESVFRSFVVDGD
FLSDTPEALINAGDFHGLQVLGVVVDKESYFLVYGAPGSKDNESLSIQAQFLAGVR
VGVPOASDLAAEAVVLYHTDNLNPDPAQLREAMDVVDGHNVCVPAQLAQRLAAQ
ARVAYIFEHRASTLSWPLMGVPHGYEIEFIFGLPLESLNTAEERFAQRLMRYW
ANFATGDPNDPRDPKVPQWPPYTAGAQYVSLDLRLPLEVRGLRAQACAFWNRFLPK
LLSATKAPSTCSGPAGEAARPRPGLSLLLLLLLLLRLLRL"
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/note="ACHE t-form; encoded by exon 4 spliced to exon 6"
/codon_start=1
/product="acetylcholinesterase collagen-tailed or globular
form precursor"
/protein_id="AAC08995.1"
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YDGRFLAQAGTIVLSMYRVGAFGLALPGSREAPGVNGLDQRLALQWQDNVATF
GGDPMSTVLFSGSAGASVGMHLLSPFSGRLGFLHRAVLQSGAPNGVATVGVGEARRA
TLLARLVGCPGGAGNDTELVAQLTRPAQDLVDHEWHVLPQESVFRSFVVDGD
FLSDTPEALINAGDFHGLQVLGVVVDKESYFLVYGAPGSKDNESLSIQAQFLAGVR
VGVPOASDLAAEAVVLYHTDNLNPDPAQLREAMDVVDGHNVCVPAQLAQRLAAQ
ARVAYIFEHRASTLSWPLMGVPHGYEIEFIFGLPLESLNTAEERFAQRLMRYW
ANFATGDPNDPRDPKVPQWPPYTAGAQYVSLDLRLPLEVRGLRAQACAFWNRFLPK
LLSATKAPSTCSGPAGEAARPRPGLSLLLLLLLRLLRL"
723 a 1256 c 1205 g 772 t 2 others
BASE COUNT
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-1 x AF053485 ..
Align seg 1/1 to: AF053485 from: 1 to: 3958

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3817 GCAGATTCACCGCTGCAGCTCTACATGCTGCACGTGGAAG 3858

seq_name: gb_pr3:HUMACHEB

seq_documentation_block:
LOCUS HUMACHEB 4185 bp DNA PRI 23-JUN-1995
DEFINITION Homo sapiens acetylcholinesterase (ACHE) gene, exons 2-6.
ACCESSION U42812
VERSION U42812.1 GI:854682
KEYWORDS acetylcholinesterase.
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for yf blood group polymorphism
JOURNAL Am. J. Hum. Genet. 52 (5), 928-936 (1993)
MEDLINE 93256075
REFERENCE 2 (bases 1 to 4185)
AUTHORS Bartels,C.F., Morlearty,P.L., Becker,R.E., Robbs,R.S.,
Sorenson,R.C., Mountjoy,C.P. and Lockridge,O.
TITLE Polymorphic sites in the acetylcholinesterase gene of patients with
Alzheimer's disease
JOURNAL Unpublished (1995)
FEATURES Location/Qualifiers

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alignment_block:
US-09-155-076-1 x HSAF002993/rev

Align seg 1/1 to reverse of: HSAF002993 from: 1 to: 34921

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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6975 GCCGAGTTCACCGCTGAGCTCTACATGTCACACTGGGAG 6934

seq_name: gb_htg29:AC011895

seq_documentation_block:
LOCUS AC011895 175155 bp DNA HTG 21-APR-2000
DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC011895
VERSION AC011895.3 GI:7630854
KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 175155)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 175155)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Apr 21, 2000 this sequence version replaced gi:6136444.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0126L15
----- Summary Statistics -----
Sequencing vector: M13; 74%
Sequencing method: plasmid; 26%
Chemistry: Dye-primer ET; 67% of reads
Assembly: Dye-terminator Big Dye; 33% of reads
Consensus quality: 173580 bases at least Q40
Consensus quality: 173920 bases at least Q30
Consensus quality: 174136 bases at least Q20
Insert size: 184000; agarose-fp
Insert size: 174955; sum-of-contigs
Quality coverage: 7.01 in Q20 bases; agarose-fp
Quality coverage: 7.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 28804: contig of 28804 bp in length
* 28805 28904: gap of unknown length
* 93340 28905: contig of 64436 bp in length
* 93341 93440: gap of unknown length
* 93441 175155: contig of 81715 bp in length.
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* Location/Qualifiers
* 1. 175155
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="7"
* /clone="RP11-126L15"

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ORIGIN

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Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AC011895/rev

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1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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135235 GCCGAGTTCACCGCTGAGCTCTACATGTCACACTGGGAG 135194

seq_name: gb_ov:AF030422

seq_documentation_block:
LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997
DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit
precursor gene, complete cds.
ACCESSION AF030422
VERSION AF030422.1 GI:2613035
KEYWORDS electric eel.
SOURCE Electrophorus electricus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;
Gymnotidae; Electrophoridae; Electrophorus.
REFERENCE 1 (bases 1 to 4472)
AUTHORS Simon,S. and Massoulié,J.
TITLE Cloning and expression of acetylcholinesterase from Electrophorus
JOURNAL J. Biol. Chem. (1997) In press
REFERENCE 2 (bases 1 to 4472)
AUTHORS Simon,S. and Massoulié,J.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-1997) Neurobiology, Ecole Normale Supérieure, 45
Rue d'Ulm, Paris 75005, France
FEATURES
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1. 4472
/organism="Electrophorus electricus"
/db_xref="taxon:8005"
118..186
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/note="type T catalytic subunit"
/codon_start=1
/product="acetylcholinesterase catalytic subunit
precursor"
/protein_id="AAB86606.1"
/db_xref="GI:2613036"
/translation="MKILDALLFPVIFIMEFHLSIAQDPELTIMRLGVOGTRLP
VPDRSHVIAFLGIPFAEPPLGKMRKPEPKPNDVDFDADYPSACQVVDYSYGF
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AHSEKVVVSNMYVSAFGLANGSAEAFNVGLLDQRLALQVQDNHFFGNGPKQ
VTFESAGAAVGMHLLSPDSRKFTRAILQSGVPGPWRVTSFDEARRRAIKLGR
VCPDNDTDLIDLRKSPQDLIDQEWLVPSGLFRFSFVFDGVVFPDTPPEAML
NSGNFKDTQILLGVNNEGSFYLLTYPAGPSKDNESLITREDFLOGVKMSVPHANEIG
LEAVILOYTDWMDENPKNREAMDIVGDHNVVCPLOHFAKMYAOYSILOGTGTAS
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/product="acetylcholinesterase catalytic subunit
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join(187..1525,1694..1886,2052..2230,3582..3700)
/note="acetylcholinesterase catalytic subunit"
BASE COUNT 1234 a 904 c 983 g 1351 t
ORIGIN

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139 GAGTTTCATCGGTGGAGTTCTCATGATGATGCACTGGAAG 177

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  Ratio: 6.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 92.857

alignment_block:
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1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
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3614 GCAGAGTTCACCGAGTTCATGATGATGCACTGGAAG 3655

seq_name: gb_ov:TMACHE2

seq_documentation_block:
  LOCUS TMACHE2 605 bp mRNA VET 14-JUL-1995
  DEFINITION Torpedo marmorata mRNA fragment for acetylcholinesterase C-term.
  (pACHE2).
  ACCESSION X13172
  VERSION X13172.1 GI:64416
  KEYWORDS acetylcholinesterase; alternative splicing.
  SOURCE marbled electric ray.
  ORGANISM Torpedo marmorata
  Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
  Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.
  Sikorav,J.L., Duval,N., Anselmet,A., Bon,S., Krejci,E., Legay,C.,
  Osterlund,M., Reimund,B. and Massoulié,J.
  TITLE Complex alternative splicing of acetylcholinesterase transcripts in
  Torpedo electric organ; primary structure of the precursor of the
  glycolipid-anchored dimeric form
  JOURNAL ENBO J. 7 (10), 2983-2993 (1988)
  MEDLINE 89030590
  COMMENT See also x13173, x13174 and x05497
  DATA kindly reviewed (24-May-1989) by Massoulié J.
  FEATURES
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        /tissue_type="electric organ."
        /clone="pACHE2"
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        <1..225
          /codon_start=1
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          /protein_id="CAA31570.1"
          /db_xref="GI:64417"
          /db_xref="SWISS-PROT:P07692"
          /translation="FIDLNTEPIKQRLRVQMCFVFNQFLPKLLNATETIDEAEROW
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        104..>605
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    BASE COUNT 127 a 228 c 117 g 133 t
    ORIGIN

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  Ratio: 6.154       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 92.308

alignment_block:
  US-09-155-076-1 x TMACHE2 ..
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2 GluPheHisArgTrpSerTyrMetValHisTrpLys 14
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OM of: US-09-155-076-1 to: N_Geneseq_36.* out_format : pfs

Date: Sep 13, 2000 2:58 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-DB=N_Geneseq_36 -OFFMT=fastap -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=100000 -USER=US09155076_CGNI_1_75
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Search information block:

Query: US-09-155-076-1

Query length: 14

Database: N_Geneseq_36.*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.680000

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N_Geneseq_36:Q09002	+	87.00	228.95	3,8e+05	2256
N_Geneseq_36:Q02496	+	62.00	156.13	0,4270	2400
N_Geneseq_36:N60111	+	62.00	155.96	0,4364	2445
N_Geneseq_36:Q48393	+	62.00	155.96	0,4364	2445
N_Geneseq_36:V74454	+	55.00	122.57	31,64	10320
N_Geneseq_36:V68847	+	50.50	125.94	20,54	1722
N_Geneseq_36:V29987	+	50.50	125.94	20,54	1722
N_Geneseq_36:V68836	+	50.50	112.46	115,62	7515
N_Geneseq_36:V29985	+	50.50	112.46	115,62	7515
N_Geneseq_36:V21209	+	49.00	83.59	4,7e+03	110000
N_Geneseq_36:V26068	+	48.00	109.21	175,51	4868
N_Geneseq_36:V94023	+	48.00	107.95	206,25	5586
N_Geneseq_36:V52253	+	48.00	105.66	276,50	7172
N_Geneseq_36:Q04960	+	47.50	105.45	283,99	6265
N_Geneseq_36:V60844	+	47.00	114.69	86,85	1948
N_Geneseq_36:Q04313	+	46.50	117.68	59,22	1200
N_Geneseq_36:V78805	+	46.00	129.13	13,64	293
N_Geneseq_36:V13398	+	46.00	115.32	80,14	1326
N_Geneseq_36:V59642	+	45.00	107.00	232,81	2400
N_Geneseq_36:V33247	+	45.00	90.94	1,8e+03	13907
N_Geneseq_36:V53431	+	44.00	112.40	116,56	970
N_Geneseq_36:V79452	+	44.00	110.83	142,60	1152
N_Geneseq_36:Q040502	+	44.00	107.55	217,03	1648
N_Geneseq_36:V62067	+	44.00	104.06	339,75	2415
N_Geneseq_36:V70137	+	44.00	95.15	1,1e+03	6393
N_Geneseq_36:Q24980	+	44.00	94.20	1,2e+03	7100
N_Geneseq_36:Q047380	+	44.00	88.84	2,4e+03	12752
N_Geneseq_36:V53431	+	43.00	109.55	168,04	966
N_Geneseq_36:N81756	+	43.00	105.46	283,75	1510
N_Geneseq_36:Q02426	+	43.00	104.48	321,80	1691
N_Geneseq_36:Q085245	+	43.00	95.80	979,90	4344
N_Geneseq_36:Q056782	+	43.00	95.80	979,90	4344
N_Geneseq_36:V99986	+	43.00	95.76	984,14	4360
N_Geneseq_36:T44068	+	43.00	94.27	1,2e+03	5132
N_Geneseq_36:V74474	+	43.00	91.13	1,8e+03	7237
N_Geneseq_36:X13176	+	43.00	79.58	7,8e+03	2580
N_Geneseq_36:X12956	+	43.00	120.40	41,79	215
N_Geneseq_36:T51174	+	42.00	114.81	85,54	396
N_Geneseq_36:Q06004	+	42.00	108.45	193,42	794
N_Geneseq_36:X00920	+	42.00	108.45	193,42	794

N_Geneseq_36:Q12851 + 42.00 108.14 201.16 821 ! A.niger PGII promoter, signa
N_Geneseq_36:Q36662 - 42.00 100.05 568.22 1990 ! Full length GP01 cDNA. DNA
N_Geneseq_36:Q07171 - 42.00 96.39 907.75 2967 ! Natural resistance-associat
N_Geneseq_36:T05501 + 42.00 96.22 928.24 3024 ! Bfrr1-PvuII fragment contg. a

seq_name: N_Geneseq_36:Q05999

seq_documentation_block:

ID Q05999 standard; DNA; 1800 BP.

AC Q05999;

DT 16-JAN-1991 (first entry)

DE Sequence encoding foetal human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

KW megakaryocytopoiesis; ovarian cancer; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 1..1500

FT 3'utr 1501..1800

FT /*tag= a

FT /*tag= b

PN EP-388906-A.

PD 26-SEP-1990.

PF 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS) YISSUM RES DEV CO.

PI Soreq H, zakut H;

PI WPI; 90-291865/39.

DR P-PSDB; R06990.

PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -
for treatment of organo-phosphorous poisoning and diagnosis of haemo-
cytopenic disorders and ovarian carcinomas.

PS Disclosure; Fig 1c; 47pp; English.

CC hACHE is useful as an active pharmacological component for the

CC prophylaxis and treatment of organophosphorous poisoning, and

CC post-surgical apnea due to succinylcholine administration.

CC cDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

CC Bases given as N are obscured in the patent specification.

CC Sequence 1800 BP; 330 A; 602 C; 539 G; 326 T;

alignment_scores:

Quality: 87.00 Length: 14

Ratio: 6.214 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x Q05999 ..

Align seg 1/1 to: Q05999 from: 1 to: 1800

1 AlagluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

1414 GCCGAGTCCAGCTGAGCTCTACATCGTCACTGGAAG 1455

seq_name: N_Geneseq_36:Q05998

seq_documentation_block:

ID Q05998 standard; DNA; 2253 BP.

AC Q05998;

DT 16-JAN-1991 (first entry)

DE Sequence encoding human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

KW megakaryocytopoiesis; ovarian cancer; ds.

OS Homo sapiens.

PN EP-388906-A.

PD 26-SEP-1990.

PF 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS) YISSUM RES DEV CO.

PI Soreq H, zakut H;

PI WPI; 90-291865/39.

DR P-PSDB; R06999.

PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -
 PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
 PS cytopoietic disorders and ovarian carcinomas.

CC Gene product is useful as an active pharmacological component for the
 CC prophylaxis and treatment of organophosphorous poisoning, and post-
 CC surgical apnea due to succinylcholine administration.
 CC cDNA probe to the sequence may be used in diagnosis of various
 CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.
 SQ Sequence 2253 BP; 390 A; 740 C; 694 G; 429 T;

alignment_scores:
 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x Q05998 ..

Align seg 1/1 to: Q05998 from: 1 to: 2253

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
 |||||
 1912 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACGTGGAAG 1953

seq_name: N_Geneseq_36:Q99002

seq_documentation_block:

ID Q99002 standard; DNA; 2256 BP.
 AC Q99002;
 DT 31-MAR-1996 (first entry)
 DE Human acetylcholinesterase (AChE) gene.
 KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;
 KW chromosome-7q22; acetylcholine-hydrolyzing enzyme; ss.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT cds 160..2206
 FT /*tag= a

PN W09523158-A1.

PD 31-AUG-1995.

PF 28-FEB-1995; U02806.

PR 28-FEB-1994; US-202755.

PR 09-JAN-1995; US-370156.

PA (KOHN/) KOHN K I.

PA (YISS) YISSUM RES & DEV CO.

PI Shani M, Soreq H, Zakut H;

DR WPI; 95-311499/40.

DR P-PSDB; R80726.

PT Alternative forms of human acetyl cholinesterase (ChE) gene -
 PT expressed in transgenic animal assay system for evaluating anti-ChE
 PT activity of organo:phosphate(s), etc. or as model of ChE imbalance

PS Claim 3; Fig.1A; 5pp; English.

CC This DNA sequence encoding human acetylcholinesterase is useful

CC for producing transgenic animals which express AChE. The

CC transgenic animals are in turn useful as an assay system for

CC determining the anti-ChE activity of organophosphates, carbamates,

CC anti-ChE drugs, plant glycoalkaloids and snake venoms. This gene

CC contains a promoter region, 6 exons (E1 to E6) and 4 introns (I1-

CC I4).

SQ Sequence 2256 BP; 390 A; 757 C; 680 G; 429 T;

alignment_scores:
 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-1 x Q99002 ..

Align seg 1/1 to: Q99002 from: 1 to: 2256

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
 |||||
 1915 GCCGAGTTCACCGCTGGAGCTCTACATGTCGACGTGGAAG 1956

seq_name: N_Geneseq_36:Q42496

seq_documentation_block:

ID Q42496 standard; cDNA; 2400 BP.

AC Q42496;

DT 06-OCT-1993 (first entry)

DE Full-length human pseudocholinesterase gene.

KW butylcholinesterase; acylcholine acylhydrolase; EC3.1.1.8; psi-CHE;

KW pseudo-ChE; neurotransmitter; organophosphorus insecticide; OP-poison;

KW antidote; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 76..1884

FT /*tag= a

FT /note= "full-length ChE gene"

FT signal_peptide 76..147

FT /*tag= b

FT /note= "putative leader peptide"

PN US5215909-A.

PD 01-JUN-1993.

PF 18-JUN-1986; 875737.

PR 21-JUN-1986; US-875737.

PR 18-AUG-1987; US-087724.

PR 15-AUG-1990; US-572911.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Soreq H;

DR WPI; 93-188509/23.

DR P-PSDB; R37442.

PT Recombinant human gene encoding human pseudo-cholinesterase -

PT used to treat organo-phosphorus poisoning

PS Disclosure; Columns 33-40; 34pp; English.

CC A cDNA library prepared from foetal brain mRNA was screened with

CC degenerate probe pools based on the organophosphorus binding site of

CC cholinesterases. A 764 nucleotide insert (designated PchE12) was

CC isolated from one positive clone and sequenced. This insert (Q42495),

CC containing an ORF large enough to code for about half the subunit

CC size of human cholinesterase, was used as a probe to obtain the full-

CC length pseudocholinesterase sequence (Q42496).

SQ Sequence 2400 BP; 794 A; 419 C; 469 G; 718 T;

alignment_scores:

Quality: 62.00 Length: 14

Ratio: 5.167 Gaps: 0

Percent Similarity: 85.714 Percent Identity: 64.286

alignment_block:

US-09-155-076-1 x Q42496 ..

Align seg 1/1 to: Q42496 from: 1 to: 2400

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
 |||||
 1792 GCAGATTCACCGCTGGACACATTACATGATGACGTGGAAG 1833

seq_name: N_Geneseq_36:N60111

seq_documentation_block:

ID N60111 standard; cDNA; 2445 BP.

AC N60111;

DT 27-JUN-1991 (first entry)

DE Sequence encoding a protein having human cholinesterase (ChE)

DE activity.

KW Organophosphorous poisoning; therapy; prophylaxis; diagnosis;

OS pseudocholinesterase deficiency; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT cds 1..1908

FT /*tag= a


```

PR 05-JAN-1996: US-009861.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
PI Rosen CA;
DR WPI: 97-374922/35.
PT polynucleotide(s) and proteins derived from Staphylococcus aureus
PT stored on computer readable medium and used in the production of
PT anti-S.aureus vaccines
PS Claim 1; Page 745-750; 327pp; English.
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
CC the S.aureus DNA sequences allows putative functions to be assigned so
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC industrial importance can be obtained. Specifically, sequences which are
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC polypeptides can also be used in a kit for the immunodetection of
CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.
SQ Sequence 10320 BP; 3071 A; 1967 C; 1531 G; 3449 T;

alignment_scores:
  Quality: 55.00 Length: 11
  Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 45.455

alignment_block:
US-09-155-076-1 x V74454/rev ..

Align seg 1/1 to reverse of: V74454 from: 1 to: 10320

3 PheHisArgTrpSerSerTyrMetValHisTrp 13
:::|||||:|||||:|||||:|||||:
908 TACCACCAATGGACAAAGTATTGTACATTGG 876

seq_name: N_Geneseq_36:T68847

seq_documentation_block:
ID T68847 standard; DNA; 1722 BP.
AC T68847;
DE 30-JAN-1998 (first entry)
KW Photorhabdus luminescens insect toxin TcbA11.
KW Insecticide; insect; toxin; pest control; biological control;
KW Photorhabdus luminescens; TcbA; Southern corn rootworm;
KW Colorado potato beetle; Western corn rootworm; meal worm;
KW boll weevil; turf grub; Coleoptera; beet armyworm; black cutworm;
KW cabbage looper; codling moth; corn earworm; European corn borer;
KW tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera;
KW Diptera; Dictyoptera; Acarina; Homoptera; ds.
OS Photorhabdus luminescens strain W-14 (ATCC 55397).
PN WO9717432-A1.
PD 15-MAY-1997.
PF 06-NOV-1996; U18003.
PR 28-AUG-1996; US-705484.
PR 06-NOV-1995; US-007255.
PR 28-FEB-1996; US-608423.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
PI Blackburn MB, Bowen DJ, Cliche TA, Ensign JC, Fatig R;
PI French-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL;
PI Petell J, Roberts JL, Rocheleau TA, Schoonover S;
PI Strickland JA;
DR WPI: 97-281022/25.
DR P-PSDB: W18303.
PT Photorhabdus sp. insecticidal protein toxins and DNA encoding them -

can be genetically engineered into insect larvae food and plants for
insect control
Claim 38; Page 229-231; 276pp; English.
This genomic DNA sequence encodes the 62.9 kDa TcbA11 insecticidal
toxin protein (see W17899) of Photorhabdus luminescens W-14.
It is derived from a full-length clone (see T68836) obtained from a
genomic library. A 280.6 kDa protein (see W17871) is processed
proteolytically into TcbA11 (see W18302) and TcbA11 components.
Claimed toxins of P. luminescens (see W17871, W17884-89, W17899-900,
W18301-06) can be produced by recombinant DNA methods and applied to,
or genetically engineered into, insect larvae food and plants for
insect control. The Photorhabdus toxins are particularly effective
against Southern corn rootworm, Colorado potato beetle, Western corn
rootworm, meal worm, boll weevil and turf grub (Coleoptera), beet
armyworm, black cutworm, cabbage looper, codling moth, corn earworm,
European corn borer, tobacco hornworm and tobacco budworm
(Lepidoptera), and are also active against insects of the orders
Hymenoptera, Diptera, Dictyoptera, Acarina and Homoptera. (All
claimed).
SQ Sequence 1722 BP; 461 A; 368 C; 446 G; 447 T;

alignment_scores:
  Quality: 50.50 Length: 14
  Ratio: 4.208 Gaps: 1
Percent Similarity: 85.714 Percent Identity: 57.143

alignment_block:
US-09-155-076-1 x T68847 ..

Align seg 1/1 to: T68847 from: 1 to: 1722

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||:|||||:|||||:|||||:
1187 GCACGGTTTCAT...TGGCAGTGGTTTATGATTCAGTGGAAG 1225

seq_name: N_Geneseq_36:V29987

seq_documentation_block:
ID V29987 standard; DNA; 1722 BP.
AC V29987;
DE 07-AUG-1998 (first entry)
DE tcbA11 gene from the tcb genomic region encoding protein TcbA.
KW Photorhabdus luminescens W-14; nematode; symbiotic;
KW Heterorhabditis; tca; tcb; tcc; tcd; insecticidal activity; toxin;
KW Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina;
KW Homoptera; Southern; Western corn rootworm; Colorado potato beetle;
KW mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;
KW cabbage looper; codling moth; corn earworm; European corn borer;
KW Tobacco hornworm; budworm; ds.
OS Photorhabdus luminescens.
FH Key Location/Qualifiers
FT CDS 1..1722
FT /*tag= a
FT WO9808932-A1.
PN 05-MAR-1998.
PD 05-MAY-1997; U07657.
PR 06-NOV-1996; WO-U18003.
PR 28-AUG-1996; US-705484.
PR 06-NOV-1996; US-743699.
PA (DMC ) DOWELANCO.
PA (WISC ) WISCONSIN ALUMNI RES FOUND.
PI Blackburn MB, Bowen DJ, Cliche TA, Ensign JC, Fatig R,
PI French-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL,
PI Petell J, Roberts JL, Rocheleau TA, Schoonover S,
PI Strickland JA, Sukhupinda K;
DR WPI: 98-179427/16.
DR P-PSDB: W36559.
PT Isolated toxins from Photorhabdus luminescens strains - useful for
PT control of insect pests
PS Claim 38; Pages 259-261; 321pp; English.
CC The present sequence encodes a protein named TcbA11 of the bacterium
CC Photorhabdus luminescens (W-14). This is a symbiotic bacterium of the

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alignment_scores:
  Quality: 50.50
  Ratio: 4.208
  Percent similarity: 85.714
  Percent Identity: 57.143

alignment_block:
  US-09-155-076-1 x T68836 ..
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Sequence	7515 BP;	2149 A;	1484 C;	1760 G;	2122 T;
SQ					

CC used as a selectable marker gene.
SQ Sequence 5586 BP; 1533 A; 1278 C; 1244 G; 1524 T;

alignment_scores:
Quality: 48.00 Length: 13
Ratio: 5.333 Gaps: 0
Percent Similarity: 69.231 Percent Identity: 46.154

alignment_block:
US-09-155-076-1 x T94023 ..

Align seg 1/1 to: T94023 from: 1 to: 5586

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrp 13
4169 TCAGATTATCATGTGATGAGTAGATATTGCTTCATTGG 4207

seq_name: N_Geneseq_36:V52253

seq_documentation_block:
ID_V52253 standard; DNA; 7172 BP.
AC V52253;
DE 23-OCT-1998 (first entry)
DE Streptococcus pneumoniae genome fragment SEQ ID NO:120.
KW Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
KW computer readable medium; vaccine; pharmaceutical composition; ds.
OS Streptococcus pneumoniae.
PN W09818931-A2.
PD 07-MAY-1998.
PF 30-OCT-1997; U19588.
PR 31-OCT-1996; US-029960.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
PI Kunsch CA, Rosen CA;
DR WPI: 98-272225/24.
PT Computer-readable medium with recorded Streptococcus pneumoniae
PT polynucleotide sequences - useful in diagnostic kits and assays, and
PT pharmaceutical compositions and vaccines for Streptococcus
PT pneumoniae
PS Claim 1; Page 846-850; 1409pp; English.
CC The present invention describes a computer readable medium which has
CC the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded
CC on it, or a representative fragment or a sequence at least 95% identical
CC to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1
CC to 391 (V52134 to V52524) are genomic fragments from Streptococcus
CC pneumoniae. The present invention also describes an isolated nucleic acid
CC molecule encoding a homologue of any of the fragments of the S.pneumoniae
CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
CC by a process comprising: (a) screening a genomic DNA library using as a
CC probe a target sequence defined by any of the sequences in SEQ ID NO:1
CC to 391, identifying members of the library which contain sequences
CC that hybridize to the target sequence and isolating the nucleic acid
CC molecules from the members; or (b) isolating mRNA, DNA or cDNA produced
CC from an organism, amplifying nucleic acid molecules whose nucleotide
CC sequence is homologous to amplification primers derived from the
CC fragment of the S. pneumoniae genome to prime the amplification and
CC isolating the amplified sequences. The computer readable medium can be
CC used in a computer-based system for identifying fragments of the
CC S. pneumoniae genome of commercial importance, or expression modulating
CC fragments of the S. pneumoniae genome. Products from the present
CC invention can be used in diagnosis kits and assays, and pharmaceutical
CC compositions and vaccines for S. pneumoniae.
SQ Sequence 7172 BP; 1920 A; 1699 C; 1381 G; 2172 T;

alignment_scores:
Quality: 48.00 Length: 9
Ratio: 6.000 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 66.667

alignment_block:
US-09-155-076-1 x V52253 ..

Align seg 1/1 to: V52253 from: 1 to: 7172

5 ArgTrpSerSerTyrMetValHisTrp 13
|||||:|||||:|||||:|||||
3765 CGGTGGAACCTCGTATCACATACACTGG 3791

TITLE OF INVENTION: TRANSFORMER

TITLE OF INVENTION: TRANSFORMER

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; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..78
; US-08-370-156-26

alignment_scores:
  Quality: 87.00      Length: 14
  Ratio: 6.214       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x US-08-370-156-26  ..

Align seg 1/1 to: US-08-370-156-26 from: 1 to: 1215

1 AlaGluPheHisArgTrpSerSerrTyrMetValHisTrpLys 14
|||||
874 GCCGAGTTCACCGCTGGAGCTCTACATGCTGTCACCTGGAAG 915

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-732-962A-1

seq_documentation_block:
; Sequence 1, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
; US-07-732-962A-1

alignment_scores:
  Quality: 87.00      Length: 14
  Ratio: 6.214       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x US-07-732-962A-1  ..

Align seg 1/1 to: US-07-732-962A-1 from: 1 to: 1845

1 AlaGluPheHisArgTrpSerSerrTyrMetValHisTrpLys 14
|||||
1756 GCCGAGTTCACCGCTGGAGCTCTACATGCTGTCACCTGGAAG 1797

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-06106-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
PCT-US92-06106-1

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: PCT-US92-06106-1 from: 1 to: 1845

1 AlaGluPheHisArgTyrSerTyrMetValHisTrpLys 14
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1756 GCCGAGTTCACCGCTGGAGCTCTACATGTCGCACTGGAAG 1797

seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-5

seq_documentation_block:
; Sequence 5, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: /note= "splice variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4 and 6"
US-08-318-826A-5

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-1

seq_documentation_block:
; Sequence 1, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-370-156-1

alignment_scores:
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    Ratio: 6.214       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-370-156-1 ..
Align seg 1/1 to: US-08-370-156-1 from: 1 to: 2256

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; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
; US-08-370-156-5

alignment_scores:
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-5

seq_documentation_block:
; Sequence 5, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc - "Alternatively spliced ache
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
; US-08-814-095-5

alignment_scores:
  Quality: 87.00      Length: 14
  Ratio: 6.214      Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x US-08-814-095-5  ..
  Align seg 1/1 to: US-08-814-095-5  from: 1 to: 3016

  1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
  ||||||||||||||||||||||||||||||||||||||||
  2675 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 2716

seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-6

seq_documentation_block:
; Sequence 6, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..1959
; OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4, 5 and the translated portion of Intron 4 (readthrough)"
US-08-318-826A-6

alignment_scores:
  Quality: 87.00      Length: 14
  Ratio: 6.214       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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Align seg 1/1 to: US-08-318-826A-6 from: 1 to: 3096

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seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-3

seq_documentation_block:
; Sequence 3, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.

; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..1959
; OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4, 5 and the translated portion of Intron 4 (readthrough)"
US-08-318-826A-6

alignment_scores:
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  Ratio: 6.214       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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Align seg 1/1 to: US-08-370-156-3 from: 1 to: 3096

1 AlaGlupheHisArgTrpSerSeryMetValHisTrpLys 14
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-3

seq_documentation_block:
; Sequence 3, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3096 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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Wed Sep 13 08:11:31 2000

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; DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion
; DESCRIPTION: of Intron 4 (readthrough)"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..1959
; US-08-814-095-3

alignment_scores:
    Quality: 87.00      Length: 14
    Ratio: 6.214        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
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seq_name: /cgn2_6/ptodata/2/lna/6_COMB.seq:US-08-814-095-7

seq_documentation_block:
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc - "Cosmid including ACHE
; DESCRIPTION: promoter, ACHE gene and AFS gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 22465..22537
; OTHER INFORMATION: /function= "non-translated"
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 24090..25177
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "(translation start:
; OTHER INFORMATION: 24110)"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
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; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ACHE"
; OTHER INFORMATION: /number= 3
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; NAME/KEY: exon
; LOCATION: 27005..27274
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
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; OTHER INFORMATION: /number= 4
; FEATURE:
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; OTHER INFORMATION: /number= 6
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; OTHER INFORMATION: /function= "arsenite resistance
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; OTHER INFORMATION: /number= 1
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; FEATURE:
; NAME/KEY: exon
; LOCATION: complement (33779..33963)
; OTHER INFORMATION: /gene= "AR"
; OTHER INFORMATION: /number= 3
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FEATURE:
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US-08-814-095-7
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Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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seq documentation_block:
; Sequence 9, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; DEVELOPMENTAL STAGE: fetal
; TISSUE TYPE: Brain, Liver
; POSITION IN GENOME:
; MAP POSITION: 3q26
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 160..1881
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /EC_number= 3.1.1.8
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "BCEH"
; OTHER INFORMATION: /note= "butyrylcholinesterase mature peptide"
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 76..159
; FEATURE:
; NAME/KEY: mRNA
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Wed Sep 13 08:11:31 2000

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; LOCATION: 1..2381
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1884
US-08-318-826A-9

alignment_scores:
    Quality: 62.00      Length: 14
    Ratio: 5.167        Gaps: 0
    Percent Similarity: 85.714    Percent Identity: 64.286

alignment_block:
US-09-155-076-1 x US-08-318-826A-9 ..

Align seg 1/1 to: US-08-318-826A-9 from: 1 to: 2381
1 AlaGluPheHisArgTyrSerTyrMetValHisTrpLys 14
||| ||||| ||||| ||||| ||||| ||||| |||||
1792 GCAGGATTCATCGCTGGACACATTACATGACTGGAAA 1833
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:20:22 ; Search time 18.63 Seconds
(without alignments)
46.505 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87

Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_64:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	583	2 S10712	acetylcholinesterase
2	87	100.0	584	2 S48724	acetylcholinesterase
3	87	100.0	614	2 JH0811	acetylcholinesterase
4	87	100.0	614	2 A39256	acetylcholinesterase
5	87	100.0	614	2 JH0314	acetylcholinesterase
6	80	92.0	596	1 ACRYE	acetylcholinesterase
7	80	92.0	599	1 A38868	acetylcholinesterase
8	65	74.7	767	2 S47639	acetylcholinesterase
9	62	71.3	602	1 ACHU	cholinesterase (EC
10	61	70.1	581	2 C39768	cholinesterase (EC
11	61	70.1	603	2 S70849	cholinesterase (EC
12	44	50.6	260	2 T12393	NADH dehydrogenase
13	43	48.4	516	2 S67037	SMP3 protein - yea
14	42	48.3	1792	2 T08878	supervillin p205 -
15	41	47.1	397	2 A75137	hypothetical prote
16	41	47.1	1323	2 T30253	spalt protein - mo
17	40.5	46.6	510	1 S64059	stearyl-CoA desat
18	40	46.0	90	2 PH1152	Ig heavy chain v r
19	40	46.0	184	2 JC2104	hypothetical 20.8K
20	40	46.0	245	2 S64351	hypothetical prote
21	40	46.0	450	2 A64546	hypothetical prote
22	40	46.0	1350	2 T30341	zinc finger protei
23	40	45.0	1995	2 T08166	probable membrane
24	39.5	45.4	469	2 S74825	probable Rieske ir
25	39.5	45.4	542	2 T02379	hypothetical prote
26	39	44.8	100	2 T09856	sucrose synthase (
27	39	44.8	138	1 HVMS77	Ig heavy chain pre
28	39	44.8	226	2 D49591	membrane protein M
29	39	44.8	226	2 S37434	membrane glycoprot

ALIGNMENTS

RESULT 1

S10712

acetylcholinesterase (EC 3.1.1.7) - bovine
C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 12-May-1995

C:Accession: S10712; A39734; B39734; B25650

R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, FEBS Lett. 266, 123-127, 1990

A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and A:Reference number: S10712; MUID:90306335

A:Accession: S10712

A:Molecule type: protein

A:Residues: 1-583 <DOC>

A:Experimental source: fetal serum

R:Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.

J. Biol. Chem. 266, 7481-7487, 1991

A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit A:Reference number: A39734; MUID:91210255

A:Accession: A39734

A:Molecule type: protein

A:Residues: 1-15; 'R', 17-38; 225-235, 'X', 237-244; 248-264, 'X', 266-273; 365-380; 396-404, 'X'

A:Experimental source: brain, erythrocyte

A:Accession: B39734

A:Molecule type: protein

A:Residues: 1-38 <ROZ>

A:Experimental source: fetal serum

R:Bon, S.; Chang, J.Y.; Strosberg, A.D.

FEBS Lett. 209, 206-212, 1986

A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s inesterase.

A:Reference number: A91370; MUID:87080761

A:Accession: B25650

A:Molecule type: protein

A:Residues: 'XS', 3-12 <BON>

A:Experimental source: caudate nucleus

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein

F;32-538/Domain: cholinesterase homology <CHE>

F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 87; DB 2; Length 583;

Best Local Similarity 100.0%; Pred. NO. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14

|||||

DB 555 AEFHRWSSVMVHWK 568

RESULT 2

S48724
acetylcholinesterase - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C:Accession: S48724
R:Chajlani, V.; Derr, D.; Earles, B.; Schnell, E.; August, T.
R:Jbilo, O.; L'Hermite, Y.; Talses, V.; Toutant, J.P.; Chatonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue
A:Reference number: S48724; MUID:95010096
A:Accession: S48724
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-584 <JBI>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: glycoprotein
F:32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
|||||
Db 556 AEFHRSSSYMVHWK 569

RESULT 3
JH0811
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999
C:Accession: JH0811
R:Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
J. Neurochem. 60, 337-346, 1993
A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul
A:Reference number: JH0811; MUID:93107932
A:Accession: JH0811
A:Molecule type: mRNA
A:Residues: 1-614 <LEG>
A:Cross-references: GB:S50879; NID:g262092; PIDN:AAB24586.1; PID:g262093
A:Experimental source: striatum
C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
F:63-569/Domain: cholinesterase homology <CHE>
F:100-127,288-303,440-560/Disulfide bonds: #status predicted
F:234,365,478/Active site: Ser, Glu, His #status predicted
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
|||||
Db 586 AEFHRSSSYMVHWK 599

RESULT 4
A39256
acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
C:Species: Homo sapiens (man)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999
C:Accession: A39256; S03959
R:Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
A:Title: Molecular cloning and construction of the coding region for human acetylcholine
A:Reference number: A39256; MUID:91088577
A:Accession: A39256

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
|||||
Db 586 AEFHRSSSYMVHWK 599

RESULT 6
ACRYE
acetylcholinesterase (EC 3.1.1.7) precursor, 11s form - Pacific electric ray
N:Alternate names: acetylcholinesterase, asymmetric form
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 26-Feb-1999

A:Molecule type: mRNA; DNA
A:Residues: 1-614 <SOR>
A:Cross-references: GB:M5040; NID:g177974; PIDN:AAA68151.1; PID:g177975
A:Note: This sequence represents composite of clones including clone ABGACHE from adu
nce should represent an authentic brain splice form
R:Chajlani, V.; Derr, D.; Earles, B.; Schnell, E.; August, T.
FBS Lett. 247, 279-282, 1989
A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a
A:Reference number: S03959; MUID:89232136
A:Accession: S03959
A:Molecule type: protein
A:Residues: 256-266, 'Y', 268-273:306-308, 'X', 310-313, 'X', 315-316, 'D', 318-323, 'D', 325-3
Y, 532-551 <CHE>
A:Experimental source: erythrocytes
A:Note: This form was a disulfide-linked homodimer
C:Genetics:
A:Gene: GDB:ACHE; YT
A:Cross-references: GDB:118746; OMIM:100740
A:Map position: 7q22-7q22
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati
F:63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
|||||
Db 586 AEFHRSSSYMVHWK 599

RESULT 5
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999
C:Accession: JH0314
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte
A:Reference number: JH0314; MUID:90380429
A:Accession: JH0314
A:Molecule type: mRNA
A:Residues: 1-614 <RAC>
A:Cross-references: EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845
A:Experimental source: brain
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-614/Product: acetylcholinesterase #status predicted <MAT>
F:63-569/Domain: cholinesterase homology <CHE>
F:100-127,288-303,440-560/Disulfide bonds: #status predicted
F:234/Active site: Ser #status predicted
F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSSYMVHWK 14
|||||
Db 586 AEFHRSSSYMVHWK 599

C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.;
 Nature 319, 407-409, 1986
 A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
 A;Reference number: A00773; PMID:86118676
 A;Accession: A00773
 A;Molecule type: mRNA
 A;Residues: 1-596 <SCH>
 A;Cross-references: GB:X03439; NID:964389
 A;Experimental source: electric organ
 A;Note: Parts of this sequence, including the amino and carboxyl ends of the mature protein
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.;
 Fed. Proc. 45, 2976-2981, 1986
 A;Title: Primary structure of acetylcholinesterase: implications for regulation and function
 A;Reference number: A60820; PMID:87054662
 A;Accession: A60820
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 22-596 <SC2>
 R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase
 A;Reference number: A92701; PMID:89066695
 A;Accession: A31962
 A;Molecule type: mRNA
 A;Residues: 1-23 <SC3>
 A;Cross-references: EMBL:X03439; NID:964389
 A;Experimental source: clones AChE-11 and AChE-18
 A;Note: revision to sequence A00773
 A;Accession: B31962
 A;Molecule type: DNA; mRNA
 A;Residues: 499-565 <SC4>
 A;Cross-references: GB:X03439; NID:964389
 A;Experimental source: clone AChE-1
 R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase
 A;Reference number: A23902; PMID:86008285
 A;Accession: A23902
 A;Molecule type: protein
 A;Residues: 22, B', 24-45; 214-237 <MAC>
 A;Note: active site Ser identification
 R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo
 A;Reference number: A41117; PMID:9129672
 A;Accession: B41117
 A;Molecule type: protein
 A;Residues: 100-108 <KRE>
 A;Note: substrate binding site
 R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A;Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase
 A;Reference number: PS0113; PMID:90166618
 A;Accession: S15677
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 557-596 <MAU>
 A;Cross-references: EMBL:X56516
 R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A;Title: Profile of the disulfide bonds in acetylcholinesterase.
 A;Reference number: A43099; PMID:87008586
 A;Contents: annotation; disulfide bonds
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 Science 253, 872-879, 1991
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 A;Reference number: A50061; PDB:1ACE
 A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
 A;Reference number: A43098; PMID:91343928
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of

C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with
 holinesterase occurs on the outer surfaces of cell membranes, including those of eryt
 C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer
 C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
 F:51-551/Domain: cholinesterase homology <CHE>
 F:80,478,554/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:88-115,275-286,423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Trp) #status experimental
 F:221/Active site: Ser #status experimental
 F:348,461/Active site: Glu, His #status predicted
 F:437/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:593/Disulfide bonds: interchain #status experimental

Query Match 92.08; Score 80; DB 1; Length 596;
 Best Local Similarity 92.3%; Pred. No. 5.9e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHWK 14
 |||||:|||||
 Db 569 EFRWSSYVHWK 581

RESULT 7
 A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C;Species: Torpedo marmorata (marbled electric ray)
 C;Date: 23-Apr-1993 #sequence-revision 15-Nov-1996 #text-change 11-Jun-1999
 C;Accession: A38868; A29682; S15696; A25650
 R;Massoulié, J.; Bon, S.
 submitted to the EMBL Data Library, June 1992
 A;Reference number: A38868
 A;Accession: A38868
 A;Molecule type: mRNA
 A;Residues: 1-599 <MAS>
 A;Cross-references: EMBL:X05497; NID:964414; PIDN:CAA29047.1; PID:964415
 R;Sikorav, J.L.; Krejci, E.; Massoulié, J.
 EMBO J. 6, 1865-1873, 1987
 A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure
 A;Reference number: A29682; MUID:88004392
 A;Accession: A29682
 A;Molecule type: mRNA
 A;Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>
 A;Cross-references: EMBL:X05497
 R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund,
 EMBO J. 7, 2983-2993, 1988
 A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo
 A;Reference number: S01293; MUID:89030590
 A;Accession: S15696
 A;Molecule type: mRNA
 A;Residues: 526-599 <SI2>
 A;Cross-references: EMBL:X13172; NID:964416; PIDN:CAA31570.1; PID:964417
 A;Experimental source: clone PACHE2
 R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
 FEBS Lett. 209, 206-212, 1986
 A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s
 inesterase.
 A;Reference number: A91370; MUID:87080761
 A;Accession: A25650
 A;Molecule type: protein
 A;Residues: 25-40, 'G', 42-47 <BON>
 C;Genetics:
 A;Gene: AChE
 C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-599/Product: acetylcholinesterase #status predicted <MAT>
F:54-554/Domain: cholinesterase homology <CHE>
F:83,440,481,557/Binding site: carboxylate (Asn) (covalent) #status predicted
F:91,118,278-289,426-545/Disulfide bonds: #status predicted
F:224,351,464/Active site: Ser, Glu, His #status predicted
F:596/Disulfide bonds: interchain #status predicted

Query Match 92.0%; Score 80; DB 1; Length 599;
Best Local Similarity 92.3%; Pred. No. 5.9e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHWK 14

Db 572 EFRWSSYVHWK 584

RESULT 8

acetylcholinesterase (EC 3.1.1.7) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C:Accession: S47639
R:Randall, W.R.; Rimer, M.; Gough, N.R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and brain
A:Reference number: S47639; MUID:94325359
A:Accession: S47639
A:Molecule type: mRNA
A:Residues: 1-767 <RAN>
A:Cross-references: EMBL:U03472; NID:9623031; PID:g424115
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match 74.7%; Score 65; DB 2; Length 767;
Best Local Similarity 76.9%; Pred. No. 0.015;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EFRWSSYVHWK 14

Db 740 EFRWSSYVGRWR 752

RESULT 9

cholinesterase (EC 3.1.1.8) precursor - human
N:Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 02-Sep-1997
C:Accession: A33769; A26613; A33887; A34668; A00772
R:Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single copy
A:Reference number: A33769; MUID:90212557
A:Accession: A33769
A:Molecule type: DNA
A:Residues: 'MSVQSNLQAGAAASCISPKYIMFTPKLHLCRESEIN', 1-602 <ARP>
A:Cross-references: GB:M32391; GB:J02879
A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation
R:Prod'g, C.A.; Zevin-Sonkin, D.; Ghatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A:Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase
A:Reference number: A26613; MUID:87231856
A:Accession: A26613
A:Molecule type: mRNA
A:Residues: 1-133, 'D', 135-602 <PRO>
R:McInternan, C.; Adkins, S.; Chattonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A:Title: Brain cDNA clone for human cholinesterase.
A:Reference number: A33887; MUID:88016155

A:Accession: A33887
A:Molecule type: mRNA
A:Residues: 'MSVQSNLQAGAAASCISPKYIMFTPKLHLCRESEIN', 1-602 <MCT>
A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for translation
R:Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Sp
Am. J. Hum. Genet. 46, 934-942, 1990
A:Title: Identification of a frameshift mutation responsible for the silent phenotype
A:Reference number: A34668; MUID:90252779
A:Accession: A34668
A:Molecule type: DNA
A:Residues: 143-145, 'VSNWNIIFTCL', <NOG>
A:Note: frameshift mutant in codon for residue 145 (Gly)
R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L
J. Biol. Chem. 262, 549-557, 1987
A:Title: Complete amino acid sequence of human serum cholinesterase.
A:Reference number: A00772; MUID:87109144
A:Accession: A00772
A:Molecule type: protein
A:Residues: 29-602 <LOC>
A:Experimental source: Plasma
C:Comment: Cholinesterase is present in most cells (except erythrocytes).
C:Genetics:
A:Gene: GDB:BCHE; CHE1
A:Cross-references: GDB:120558; OMIM:177400
A:Map position: 3q26.1-3q26.2
A:Introns: 506/2; 562/1
C:Function:
A:Description: hydrolyzes acylcholines to choline and a carboxylic acid
A:Note: This cholinesterase is highly reactive with organophosphate esters
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-602/Product: cholinesterase #status experimental <MAT>
F:56-556/Domain: cholinesterase homology <CHE>
F:45,85,134,269,284,369,483,509,514/Binding site: carboxylate (Asn) (covalent) #status
F:226/Active site: Ser #status experimental

Query Match 71.3%; Score 62; DB 1; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.035;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYVHWK 14

Db 573 AGFHRWNNYMDWK 586

RESULT 10

cholinesterase (EC 3.1.1.8) - rabbit
N:Alternate names: butyrylcholinesterase
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 18-Jun-1999
C:Accession: S10255; C39768
R:Jbilo, O.; Chattonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A:Title: Complete sequence of rabbit butyrylcholinesterase.
A:Reference number: S10255; MUID:90326526
A:Accession: S10255
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-581 <JBI>
A:Cross-references: EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:e247309; PID:g137027
R:Arpagaus, M.; Chattonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;
J. Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholines
A:Reference number: A39768; MUID:91201348
A:Accession: C39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 75-215 <ARP>
A:Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
C:Genetics:

10

A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1792 <PES>
 A:Cross-references: EMBL:AF025996; NID:g2668622; PID:g2668623
 A:Experimental source: cell line MDBK (Madin Darby Bovine Kidney); ATCC CCL-22
 C:Superfamily: villin headpiece homology
 C:Keywords: actin binding; cell adhesion; membrane-associated protein
 F:1732-1792/Domain: villin headpiece homology <VHH>

Query Match 48.3%; Score 42; DB 2; Length 1792;
 Best Local Similarity 46.2%; Pred. No. 1.2e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 EFHRWSSVMVHWK 14
 :||:|:|:
 Db 1352 QFEGDAIVVWKK 1364

RESULT 15
 A75137
 hypothetical protein PAB0600 - Pyrococcus abyssi (strain Orsay)
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: A75137
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A:Reference number: A75001
 A:Accession: A75137
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-397 <KAW>
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49810.1; PID:s151570
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB0600

Query Match 47.1%; Score 41; DB 2; Length 397;
 Best Local Similarity 40.0%; Pred. No. 40;
 Matches 6; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

OY 2 EFH--RWSSVMVHWK 14
 :||:|:|:
 Db 18 DYHVKRWKEQKLHWK 32

Search completed: September 13, 2000, 02:22:33
 Job time: 131 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:42 ; Search time 10.66 Seconds
(without alignments)
40.699 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 87
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	583	1 ACES_BOVIN	P23795 bos taurus
2	87	100.0	584	1 ACES_RABIT	Q29499 oryctolagus
3	87	100.0	614	1 ACES_HUMAN	P22303 homo sapien
4	87	100.0	614	1 ACES_MOUSE	P21836 mus musculus
5	87	100.0	614	1 ACES_RAT	P37136 rattus norv
6	65	74.7	767	1 ACES_CHICK	P36196 gallus gall
7	62	71.3	602	1 CHLE_HUMAN	P06276 homo sapien
8	61	70.1	581	1 CHLE_RABIT	P21927 oryctolagus
9	61	70.1	603	1 CHLE_MOUSE	Q03311 mus musculus
10	44	50.6	746	1 NUSC_ARATH	P56752 arabidopsis
11	43	49.4	516	1 SMP3_YEAST	Q04174 saccharomyc
12	40.5	46.6	510	1 ACOL_YEAST	P21147 saccharomyc
13	40	46.0	245	1 YG24_YEAST	P33237 saccharomyc
14	40	46.0	716	1 RRP2_IARTE	P31369 influenza a
15	40	46.0	1995	1 YCX7_CHLRE	P36495 chlamydomon
16	39	44.8	138	1 HV48_MOUSE	P03980 mus musculus
17	39	44.8	507	1 SXA2_SCHPO	P32825 schizosacch
18	39	44.8	575	1 UL87_EBV	P01363 schizosacch
19	39	44.8	1237	1 YD12_SCHPO	P19127 drosophila
20	38.5	44.3	318	1 AG0D_DROME	P18930 drosophila
21	38	43.7	117	1 NUS3M_DROSA	P51940 drosophila
22	38	43.7	117	1 NUS3M_DROSA	P07705 drosophila
23	38	43.7	117	1 Y770_MYCTU	P17825 mycobacteri
24	38	43.7	295	1 Y770_MYCTU	P23998 vaccinia vi
25	38	43.7	351	1 VB19_VACCV	P25213 vaccinia vi
26	38	43.7	351	1 VB19_VACCV	P21077 vaccinia vi
27	38	43.7	353	1 VB19_VACCV	P23347 rattus norv
28	38	43.7	1234	1 B3A2_RAT	P13808 mus musculus
29	38	43.7	1237	1 B3A2_MOUSE	P48746 oryctolagus
30	38	43.7	1237	1 B3A2_RABIT	P20241 drosophila
31	38	43.7	1239	1 NRG_DROME	P52063 mycobacteri
32	37.5	43.1	285	1 YD41_MYCLE	P34849 apis mellif
33	37.5	43.1	333	1 NU2M_APILI	

34 37.5 43.1 494 1 GPPA_ECOLI
35 37 42.5 137 1 HV11_MOUSE
36 37 42.5 185 1 YH00_YEAST
37 37 42.5 327 1 DHBI_HUMAN
38 37 42.5 551 1 AAP2_NEUCR
39 37 42.5 661 1 MX1_HUMAN
40 37 42.5 686 1 FREI_YEAST
41 37 42.5 901 1 VGLB_GPCMV
42 37 42.5 1350 1 XF1N_XENLA
43 37 42.5 1357 1 YJ03_YEAST
44 36.5 42.0 1407 1 CYAA_DICDI
45 36 41.4 218 1 NUVM_NEUCR

ALIGNMENTS

RESULT 1
ACES_BOVIN STANDARD; PRT; 583 AA.
ID ACES_BOVIN
AC P23795;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACETYLCHOLINESTERASE (EC 3.1.1.7).
GN ACHE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=FETAL SERUM;
RX MEDLINE: 90306335.
RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RA "Complete amino acid sequence of fetal bovine serum
RT acetylcholinesterase and its comparison in various regions with other
RT cholinesterases.";
RL FEBS Lett. 266:123-127(1990).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR PIR: S10712; S10712.
DR HSP; P22303; 2CLJ.
DR PFAM: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLNESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle;
KW Neurotransmitter degradation; Glycoprotein.
FT ACT_SITE 203 203 BY SIMILARITY.
FT ACT_SITE 334 334 BY SIMILARITY.
FT ACT_SITE 447 447 BY SIMILARITY.
FT DISULFID 69 96 BY SIMILARITY.
FT DISULFID 257 272 BY SIMILARITY.
FT DISULFID 409 529 BY SIMILARITY.
FT DISULFID 580 580 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 265 265 POTENTIAL.
FT CARBOHYD 350 350 POTENTIAL.
FT CARBOHYD 464 464 POTENTIAL.
FT CARBOHYD 541 541 POTENTIAL.
SQ SEQUENCE 583 AA; 64238 MW; 78655017E494279F CRC64;

Query Match 100.0%; Score 87; DB 1; Length 583;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
|||||

Db 555 AEFHRSSYVHWK 568

RESULT 2
 ACES_RABBIT STANDARD; PRT; 584 AA.
 ID ACES_RABBIT Q29499;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).
 GN ACHE.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RX MEDLINE; 95010096.
 RA Jbilo O., Lhermite Y., Toutant J., Chatonnet A.;
 RT "Acetylcholinesterase and butyrylcholinesterase expression in adult
 rabbit tissues and during development.";
 RL Eur. J. Biochem. 225:115-124(1994).
 CC -1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
 CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
 CC ERYTHROCYTES.
 CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 CC SOLUBLE FORM OF ACHE.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U05036; AAA53235.1; -
 DR HSP; P22303; 2CLJ.
 DR PFAM; P00135; Coesterase; 1.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B.1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B.2; 1.
 KW Hydrolase; Serine esterase; synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein.
 FT NON_TER 1 1
 FT SIGNAL <1 1 POTENTIAL.
 FT CHAIN 2 584 ACETYLCHOLINESTERASE.
 FT ACT_SITE 204 204 BY SIMILARITY.
 FT ACT_SITE 335 335 BY SIMILARITY.
 FT ACT_SITE 448 448 BY SIMILARITY.
 FT DISULFID 70 97 BY SIMILARITY.
 FT DISULFID 258 273 BY SIMILARITY.
 FT DISULFID 410 530 BY SIMILARITY.
 FT DISULFID 581 581 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 266 266 POTENTIAL.
 FT CARBOHYD 351 351 POTENTIAL.
 FT CARBOHYD 465 465 POTENTIAL.
 SQ SEQUENCE 584 AA: 64630 NW; 2AE157F3063649FE CRC64;

Query Match 100.0%; Score 87; DB 1; Length 584;
 Best Local Similarity 100.0%; Pred. No. 6e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSYVHWK 14

|||||||

Db 556 AEFHRSSYVHWK 569

RESULT 3
 ACES_HUMAN STANDARD; PRT; 614 AA.
 ID ACES_HUMAN P22303;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
 GN ACHE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91088577.
 RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnatt A., Neville L.,
 RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
 RA Zakut H.;
 RT "Molecular cloning and construction of the coding region for human
 acetylcholinesterase reveals a G + C-rich attenuating structure.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
 CC [2]
 CC PARTIAL SEQUENCE.
 CC TISSUE-ERYTHROCYTE;
 CC MEDLINE; 89232136.
 RA Chhajlani V., Derr D., Earles B., Schmell E., August T.;
 RT "Purification and partial amino acid sequence analysis of human
 erythrocyte acetylcholinesterase.";
 RL FEBS Lett. 247:279-282(1989).
 CC [3]
 CC MUTAGENESIS OF CYS-611.
 CC MEDLINE; 92084599.
 RA Velan B., Grosfeld H., Kronman C., Leitner M., Gozes Y., Lazar A.,
 RA Flashner Y., Marcus D., Cohen S., Shaferman A.;
 RT "The effect of elimination of intersubunit disulfide bonds on the
 RT activity, assembly, and secretion of recombinant human
 RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
 RT mutant.";
 RL J. Biol. Chem. 266:23977-23984(1991).
 CC [4]
 CC MUTAGENESIS OF ACTIVE-SITE RESIDUES AND OF ASP-206 AND ASP-435.
 CC MEDLINE; 92388112.
 RA Shaffer A., Kronman C., Flashner Y., Leitner M., Grosfeld H.,
 RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
 RT "Mutagenesis of human acetylcholinesterase. Identification of
 RT residues involved in catalytic activity and in polypeptide folding.";
 RL J. Biol. Chem. 267:17640-17648(1992).
 CC [5]
 CC VARIANT BLOOD GROUP YT(B).
 CC MEDLINE; 93256075.
 RA Bartels C.F., Zelinski T., Lockridge O.;
 RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
 RT accounts for YT blood group polymorphism.";
 RL Am. J. Hum. Genet. 52:928-936(1993).
 CC -1- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -1- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.
 CC THE MOLECULAR BASIS OF THE YT(A)-YT(B)-YT2 BLOOD GROUP
 CC ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353
 CC CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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DR EMBL; M55040; AAA68151.1; -.
 DR PIR; S03959; S03959.
 DR PIR; A39256; A39256.
 DR PDB; 2CLJ; 04-MAR-98.
 DR CARBANK; CCSD:29374; -.
 DR CARBANK; CCSD:32958; -.
 DR CARBANK; CCSD:35085; -.
 DR CARBANK; CCSD:36427; -.
 DR SWISS-2DPAGE; P22303; HUMAN.
 DR MIM; 100740; -.
 DR MIM; 112100; -.
 DR PFAM; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTERASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; Polymorphism;
 KW Blood group antigen; Alternative splicing; 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 614
 FT ACT_SITE 234 234
 FT ACT_SITE 365 365
 FT ACT_SITE 478 478
 FT DISULFID 100 127
 FT DISULFID 288 303
 FT DISULFID 440 560
 FT DISULFID 611 611
 FT CARBOHYD 296 296
 FT CARBOHYD 381 381
 FT CARBOHYD 495 495
 FT VARIANT 353 353
 FT MUTAGEN 234 234
 FT MUTAGEN 365 365
 FT MUTAGEN 478 478
 FT MUTAGEN 206 206
 FT MUTAGEN 435 435
 FT MUTAGEN 611 611
 SQ SEQUENCE 614 AA; 67796 MW; B9A84C77831C302 CRC64;
 Query Match 100.0%; Score 87; DB 1; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFHRSSYMWVHK 14
 Db 586 AEFHRSSYMWVHK 599
 RESULT 4
 ACES_MOUSE STANDARD; PRT; 614 AA.
 AC P21836;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
 GN ACHE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 90380429.
 RA Rachinsky T.L., Camp S., Li Y., Ekstrom T.J., Newton M., Taylor P.;
 RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
 of alternatively spliced mRNA species.";
 RL Neuron 5:317-327(1990).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
 RX MEDLINE; 96067648.

RA EMBL; M55040; AAA68151.1; -.
 RT PIR; S03959; S03959.
 RT PIR; A39256; A39256.
 RL Cell 83:503-512(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE; 99115643.
 RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
 RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
 occluding loop in a tetrameric assembly.";
 RL J. Biol. Chem. 274:2963-2970(1999).
 CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
 CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -|- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED
 CC BY ALTERNATIVELY SPLICED MRNAS THAT ARISE FROM A SINGLE GENE.
 CC THE T (ASYMMETRIC) FORM IS SHOWN HERE.
 CC -|- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
 CC EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
 CC ACHE PREDOMINATES.
 CC -|- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
 CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
 CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
 CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
 CC ERYTHROCYTES.
 CC -|- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
 CC SOLUBLE FORM OF ACHE.
 CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X56518; CAA39867.1; -.
 DR PIR; JH0314; JH0314.
 DR PDB; 1MAH; 03-APR-96.
 DR PDB; 1MAA; 20-APR-99.
 DR MGI; 87876; ACHE.
 DR PFAM; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTERASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
 KW 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 614
 FT ACT_SITE 234 234
 FT ACT_SITE 365 365
 FT ACT_SITE 478 478
 FT DISULFID 100 127
 FT DISULFID 288 303
 FT DISULFID 440 560
 FT DISULFID 611 611
 FT CARBOHYD 296 296
 FT CARBOHYD 381 381
 FT CARBOHYD 495 495
 SQ SEQUENCE 614 AA; 68168 MW; 66E2512463C21172 CRC64;
 Query Match 100.0%; Score 87; DB 1; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFHRSSYMWVHK 14
 Db 586 AEFHRSSYMWVHK 599

Query Match 100.0%; Score 87; DB 1; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AEFHRSSYMWVHK 14
 Db 586 AEFHRSSYMWVHK 599

RESULT 5
 ID ACES_RAT STANDARD; PRT; 614 AA.
 AC P37136;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
 GN ACHE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A. (T FORM).
 RX MEDLINE; 93107932.
 RA Legay C., Bon S., Vernier P., Cousens F., Massoulie J.;
 RT "Cloning and expression of a rat acetylcholinesterase subunit:
 generation of multiple molecular forms and complementarity with a
 Torpedo collagenic subunit.";
 RL J. Neurochem. 60:337-346(1993).
 [2]
 RP SEQUENCE FROM N.A. (H AND R FORMS).
 RX MEDLINE; 93114454.
 RA Legay C., Bon S., Massoulie J.;
 RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
 acetylcholinesterase.";
 RL FEBS Lett. 315:163-166(1993).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGEN-
 TAILED), WHICH DIFFER IN THEIR C-TERMINUS, ACCOUNT FOR ALL TYPES
 OF KNOWN ACHE FORMS.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED
 BY ALTERNATIVELY SPLICED MRNAS THAT ARISE FROM A SINGLE GENE.
 CC IT IS NOT KNOWN WHETHER THE R FORM REPRESENTS A FUNCTIONAL
 SPECIES. THE T (ASYMMETRIC) FORM IS SHOWN HERE.
 CC -1- TISSUE SPECIFICITY: HAS BEEN FOUND IN CENTRAL NERVOUS SYSTEM AND
 MUSCLE. FOUND IN EMBRYONIC LIVER AND SPLEEN BUT NOT IN ADULT
 LIVER.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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 DR EMBL; S50879; AAB24586.1; -.
 DR EMBL; X70140; CAA49717.1; -.
 DR EMBL; X70141; CAA49718.1; -.
 DR PIR; JH0811; JH0811.
 DR HSP; P21836; IMAH.
 DR PRAM; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 31
 FT CHAIN 32 614
 FT ACETYLCHOLINESTERASE.
 FT ACT_SITE 234 364
 FT BY SIMILARITY.
 FT ACT_SITE 365 478
 FT BY SIMILARITY.
 FT ACT_SITE 478 478
 FT BY SIMILARITY.
 FT DISULFID 100 127
 FT BY SIMILARITY.
 FT DISULFID 288 303
 FT BY SIMILARITY.
 FT DISULFID 440 560
 FT BY SIMILARITY.
 FT DISULFID 611 611
 FT INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 296 296
 FT POTENTIAL.
 FT CARBOHYD 381 381
 FT POTENTIAL.
 FT CARBOHYD 495 495
 FT POTENTIAL.

FT VARSPLIC 570 614
 FT LLSATDTLDEARQKAEFRHSSVMVHKNQFDHYSKOER
 FT CSOL -> LLSATATEVPTCTSPAHGEAARPGPALSLSL
 FT LFLFLHLSGLRWL (IN ISOFORM H).
 FT LLSATDTLDEARQKAEFRHSSVMVHKNQFDHYSKOER
 FT CSOL -> LLSATGRGQVKGQMHKAAVGTGGERGGKRR
 FT M (IN ISOFORM R).
 SQ SEQUENCE 614 AA; 68196 MW; 2EDAE7D46282E7C0 CRC64;
 Query Match 100.0%; Score 87; DB 1; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6.3e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHRWSSVMVHVK 14
 |||||
 DB 586 AEFHRWSSVMVHVK 599
 |||||
 RESULT 6
 ID ACES_CHICK STANDARD; PRT; 767 AA.
 AC P36196;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
 GN ACHE.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-MUSCLE;
 RX MEDLINE; 94325359.
 RA Randall W.R., Rimer M., Gough N.R.;
 RT "Cloning and analysis of chicken acetylcholinesterase transcripts
 from muscle and brain.";
 RL Biochim. Biophys. Acta 1218:453-456(1994).
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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 DR EMBL; U03472; AAB60456.1; -.
 DR HSP; P21836; IMAH.
 DR PRAM; PF00135; Coesterase; 2.
 DR PRINTS; PR00878; CHOLNESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
 KW Neurotransmitter degradation; Glycoprotein.
 FT SIGNAL 1 19
 FT CHAIN 20 767
 FT ACETYLCHOLINESTERASE.
 FT ACT_SITE 227 227
 FT BY SIMILARITY.
 FT ACT_SITE 520 520
 FT BY SIMILARITY.
 FT ACT_SITE 633 633
 FT BY SIMILARITY.
 FT DISULFID 94 121
 FT BY SIMILARITY.
 FT DISULFID 281 292
 FT BY SIMILARITY.
 FT DISULFID 595 713
 FT BY SIMILARITY.
 FT DISULFID 764 764
 FT INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 285 285
 FT POTENTIAL.
 FT CARBOHYD 536 536
 FT POTENTIAL.
 FT CARBOHYD 650 650
 FT POTENTIAL.
 FT CARBOHYD 725 725
 FT POTENTIAL.

FT VARIANT 98 98 D -> G (IN ATYPICAL FORM, DIBUCAINE-
RESISTANT).
/FTid-VAR_002360.
FT VARIANT 271 271 T -> M (IN FLUORIDE-1).
/FTid-VAR_002361.
FT VARIANT 358 358 L -> I (IN HYPOCHOLINESTERASEMIA).
/FTid-VAR_002362.
FT VARIANT 418 418 G -> V (IN FLUORIDE-2).
/FTid-VAR_002363.
FT VARIANT 567 567 A -> T (IN K VARIANT, WITH REDUCED ENZYME
ACTIVITY).
/FTid-VAR_002364.
SQ SEQUENCE 602 AA; 68418 MW; C9836409D9057F27 CRC64;

Query Match 71.3%; Score 62; DB 1; Length 602;
Best Local Similarity 64.3%; Pred. No. 0.031;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
I | | | | : | | : | |
Db 573 AGFHRWNNYMDWK 586

RESULT 8
CHLE_RABIT
ID CHLE_RABIT STANDARD; PRT; 581 AA.
AC P21927;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)
DE (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)
DE (PSEUDOCOLINESTERASE).
GN BCHE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=LAGOMORPHA;
RX MEDLINE; 90326526.
RA Jbilo O., Roudani S., Chatonnet A.;
RT "Complete sequence of rabbit butyrylcholinesterase.";
RL Nucleic Acids Res. 18:3990-3990(1990).
[2]
RP SEQUENCE OF 75-215 FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 91201348.
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RT Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H2(O) = CHOLINE + A
CARBOXYLIC ACID ANION.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

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DR EMBL; X52090; CAA36308.1; -.

DR EMBL; X52091; CAA36308.1; JOINED.
DR EMBL; X52092; CAA36308.1; JOINED.
DR EMBL; M62779; AAA31169.1; -.
DR PIR; S10255; S10255.
DR PIR; C39768; C39768.
DR HSP; P21836; 1MAH.
DR PRMT; PF00135; Coesterase; 1.
DR PRNTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Signal.
POTENTIAL.
FT CHAIN 1 8
FT SIGNAL 9 581
FT ACT_SITE 205 205
FT ACT_SITE 332 332
FT ACT_SITE 445 445
FT DISULFID 72 99
FT DISULFID 259 270
FT DISULFID 407 526
FT DISULFID 578 578
FT CARBOHYD 64 64
FT CARBOHYD 113 113
FT CARBOHYD 248 248
FT CARBOHYD 263 263
FT CARBOHYD 348 348
FT CARBOHYD 462 462
FT CARBOHYD 488 488
FT CARBOHYD 492 492
FT CARBOHYD 493 493
SQ SEQUENCE 581 AA; 66156 MW; FEBB199E7B32EB0A CRC64;

Query Match 70.1%; Score 61; DB 1; Length 581;
Best Local Similarity 64.3%; Pred. No. 0.042;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AEFHRWSSVMVHWK 14
I | | | | : | | : | |
Db 552 AGFHRWNNYMDWK 565

RESULT 9
CHLE_MOUSE
ID CHLE_MOUSE STANDARD; PRT; 603 AA.
AC Q03311;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE)
DE (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE)
DE (PSEUDOCOLINESTERASE).
GN BCHE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 90380429.
RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
[2]
RN SEQUENCE OF 97-237 FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 91201348.
RA Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of
butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: AN ACYLCHOLINE + H2(O) = CHOLINE + A
CARBOXYLIC ACID ANION.


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DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE SUBUNIT P2 (EC 2.7.7.48) (POLYMERASE
DE ACIDIC PROTEIN) (PA).
OS Influenza A virus (strain A/Equine/Tennessee/5/86).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90021190.
RA Okazaki K., Kawakita Y., Webster R.G.;
RT "Evolutionary pathways of the PA genes of influenza A viruses.";
RL Virology 172:601-608(1989).
CC -!- SUBUNIT: INFLUENZA RNA POLYMERASE IS COMPOSED OF THREE SUBUNITS:
CC P1 (OR PB1), P2 (OR PA), AND P3 (OR PB2).
CC -!- SIMILARITY: BELONGS TO THE INFLUENZA VIRUSES POLYMERASE PA FAMILY.
CC
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CC -----
CC EMBL: M26082; AAA3113.1; -.
CC PFAM: PF00603; Flu_PA; 1.
CC Transferrase; RNA-directed RNA polymerase.
KW SEQUENCE 716 AA; 82724 MW; 9922E3E3995B0C96 CRC64;
SQ
Query Match 46.0%; Score 40; DB 1; Length 716;
Best Local Similarity 54.5%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EPHRWSYMHV 12
DB 533 EPHWEKYCVH 543
| | | | |
| | | | |

RESULT 15
YCX7-CHLRE
ID YCX7-CHLRE STANDARD; PRT; 1995 AA.
AC P36495; Q37303.
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE 232.2 KDA PROTEIN (ORF1995) (ORF-S) (ORFA).
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97218038.
RA Boudreau E., Turmel M., Goldschmidt-Clermont M., Rochaix J.-D.,
RA Sivan S., Michaels A., Leu S.;
RT "A large open reading frame (orf1995) in the chloroplast DNA of
RT Chlamydomonas reinhardtii encodes an essential protein.";
RL Mol. Gen. Genet. 253:649-653(1997).
RN [2]
RP SEQUENCE OF 1573-1995 FROM N.A.
RC STRAIN-CW15;
RA Sivan S., Michaels A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1925-1995 FROM N.A.
RX MEDLINE: 87031585.
RA Woessner J.P., Gilham N.W., Boynton J.E.;
RT "The sequence of the chloroplast atpB gene and its flanking regions
RT in Chlamydomonas reinhardtii.";
RL Gene 44:17-28(1986).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.

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RX MEDLINE: 94207185.
RA Boudreau E., Otis C., Turmel M.;
RT "Conserved gene clusters in the highly rearranged chloroplast genomes
RT of Chlamydomonas moewusii and Chlamydomonas reinhardtii.";
RL Plant Mol. Biol. 24:585-602(1994).
CC -!- FUNCTION: ESSENTIAL FOR CELL GROWTH. MAY BE INVOLVED IN BINDING
CC CHLOROPLAST DNA TO EITHER THE CHLOROPLAST ENVELOPE OR THE
CC THYLAKOID MEMBRANE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -!- SIMILARITY: TO C.VULGARIS ORF819.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X92726; CAA63385.1; -.
CC EMBL: X76934; CAA54257.1; -.
CC PIR: S41289; S41289.
KW Chloroplast; Transmembrane.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 254 274 POTENTIAL.
FT TRANSMEM 307 327 POTENTIAL.
FT CONFLICT 1588 1588 K -> R (IN REF. 2).
SQ SEQUENCE 1995 AA; 232194 MW; E5A3F167EAF5FC8A CRC64;

Query Match 46.0%; Score 40; DB 1; Length 1995;
Best Local Similarity 60.0%; Pred. No. 17e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RWSSYMHVHK 14
DB 882 RWTYMHYK 891
| | | | |
| | | | |

Search completed: September 13, 2000, 02:24:31
Job time: 169 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:37 ; Search time 14.59 seconds
(without alignments)
14.709 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 14

Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size: 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	40	2	US-08-370-156-25
2	14	100.0	45	2	US-08-370-156-7
3	14	100.0	45	2	US-08-370-156-8
4	14	100.0	614	1	US-07-732-962A-2
5	14	100.0	614	2	US-08-370-156-2
6	14	100.0	614	3	US-08-446-100-19
7	14	100.0	614	3	US-08-446-100-20
8	14	100.0	614	3	US-08-446-100-21
9	14	100.0	614	3	US-08-446-100-22
10	14	100.0	614	3	US-08-446-100-23
11	14	100.0	614	3	US-08-446-100-24
12	14	100.0	614	3	US-08-814-095-2
13	14	100.0	614	4	PCT-US92-06106-2
14	9	64.3	575	1	US-08-348-920-1
15	9	64.3	575	1	US-08-348-920-2
16	4	28.6	10	2	US-08-556-597-145
17	4	28.6	13	2	US-08-934-222-66
18	4	28.6	13	2	US-08-933-402-66
19	4	28.6	13	2	US-09-207-621-66
20	4	28.6	13	2	US-08-532-818-66
21	4	28.6	15	1	US-08-551-128A-1
22	4	28.6	15	1	US-08-551-128A-2
23	4	28.6	15	1	US-08-133-271-5
24	4	28.6	20	1	US-08-250-789A-179
25	4	28.6	21	2	US-08-612-840A-3
26	4	28.6	27	1	US-08-384-212-4
27	4	28.6	27	2	US-08-739-819-4
28	4	28.6	32	3	US-08-954-915A-18

Sequence 1, Appli
Sequence 95, Appli
Sequence 110, App
Sequence 95, Appli
Sequence 110, App
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 17, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 1, Appli
Sequence 6, Appli
Sequence 5, Appli

29 4 28.6 38 2 US-08-612-840A-1
30 4 28.6 58 3 US-08-676-124-95
31 4 28.6 58 3 US-08-676-124-110
32 4 28.6 58 3 US-09-414-878-95
33 4 28.6 58 3 US-09-414-878-110
34 4 28.6 64 1 US-08-485-971-21
35 4 28.6 64 1 US-08-383-754-21
36 4 28.6 64 2 US-08-485-978-21
37 4 28.6 64 2 US-08-486-814-21
38 4 28.6 64 2 US-08-487-472-21
39 4 28.6 64 4 PCT-US92-00282-17
40 4 28.6 64 4 PCT-US95-08179-21
41 4 28.6 68 2 US-08-637-759B-62
42 4 28.6 68 3 US-08-871-355A-62
43 4 28.6 72 1 US-08-379-538-1
44 4 28.6 72 1 US-08-379-538-6
45 4 28.6 90 1 US-08-085-122-5

ALIGNMENTS

RESULT 1
US-08-370-156-25
Sequence 25, Application US/08370156
Patent No. 5932780

GENERAL INFORMATION:

APPLICANT: Soxeq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
NUMBER OF SEQUENCE: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: US
ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370.156

FILING DATE:

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307 (Mulford)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

Query Match 100.0%; Score 14; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.7e-10;
Matches 14; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14

Db 12 AEFHRWSSVMVHWK 25

*Search
Serge Limited*

```

RESULT 2
US-08-370-156-7
; Sequence 7, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-7

Query Match 100.0%; Score 14; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVMVHWK 14
Db 17 AEFHRSSVMVHWK 30

RESULT 3
US-08-370-156-8
; Sequence 8, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-732-962A-2

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-8

Query Match 100.0%; Score 14; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVMVHWK 14
Db 17 AEFHRSSVMVHWK 30

RESULT 4
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-732-962A-2

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Query Match 100.0%; Score 14; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | |
DB 586 AEFHRWSSYVHWK 599

RESULT 5
US-08-370-156-2
; Sequence 2, Application US/08370156
; Patent No. 5932780
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TELECOMMUNICATION INFORMATION:
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,156
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-370-156-2

Query Match 100.0%; Score 14; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | |
DB 586 AEFHRWSSYVHWK 599

RESULT 6
US-08-446-100-19
; Sequence 19, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-19

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| | | | | | | | | |
DB 586 AEFHRWSSYVHWK 599

RESULT 7
US-08-446-100-20
; Sequence 20, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-20

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 586 AEFHRWSSYMVHWK 599

RESULT 8
US-08-446-100-21
; Sequence 21, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
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; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-21

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 586 AEFHRWSSYMVHWK 599

RESULT 9
US-08-446-100-22
; Sequence 22, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-22

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYMVHWK 14
Db 586 AEFHRWSSYMVHWK 599

RESULT 10
US-08-446-100-23
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 614 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-25

Query Match 100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels

QY 1 AEFHRWSSYVHWK 14
      |||iiiiiiiiiii
DDB 586 AEFHRWSSYVHWK 599

RESULT 12
US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTRANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 NO. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055

```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 614 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
; US-08-814-095-2

Query Match          100.0%; Score 14; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

* QY 1 AEFHRWSSYVHWK 14
      |||||
Db 586 AEFHRWSSYVHWK 599

RESULT 13
PCT-US92-06106-2
; Sequence 2, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Melr
; TITLE OF INVENTION: ENZYMICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 614 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; PCT-US92-06106-2

Query Match          100.0%; Score 14; DB 4; Length 614;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
      |||||
Db 586 AEFHRWSSYVHWK 599

RESULT 14
US-08-348-920-1
; Sequence 1, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupandra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; TITLE OF INVENTION: Organophosphates
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 575 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: internal
; US-08-348-920-1

Query Match          64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSY 10
      |||||
Db 548 EFRWSSY 556

RESULT 15
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
; GENERAL INFORMATION:
; APPLICANT: Doctor, Bhupandra P.
; APPLICANT: Maxwell, Donald
; APPLICANT: Saxena, Ashima
; APPLICANT: Radic, Zoran
; APPLICANT: Taylor, Palmer
; TITLE OF INVENTION: Compositions for Use to Deactivate
; TITLE OF INVENTION: Organophosphates
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John F. Moran
; STREET: Off. of Command Judge Adv., HQ USAMRDC, Fort
```

```

; STREET: Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/348,920
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: doc348,920
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-7807
; TELEFAX: 301-619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 575 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
;
US-08-348-920-2

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Query Match      64.3%; Score 9; DB 1; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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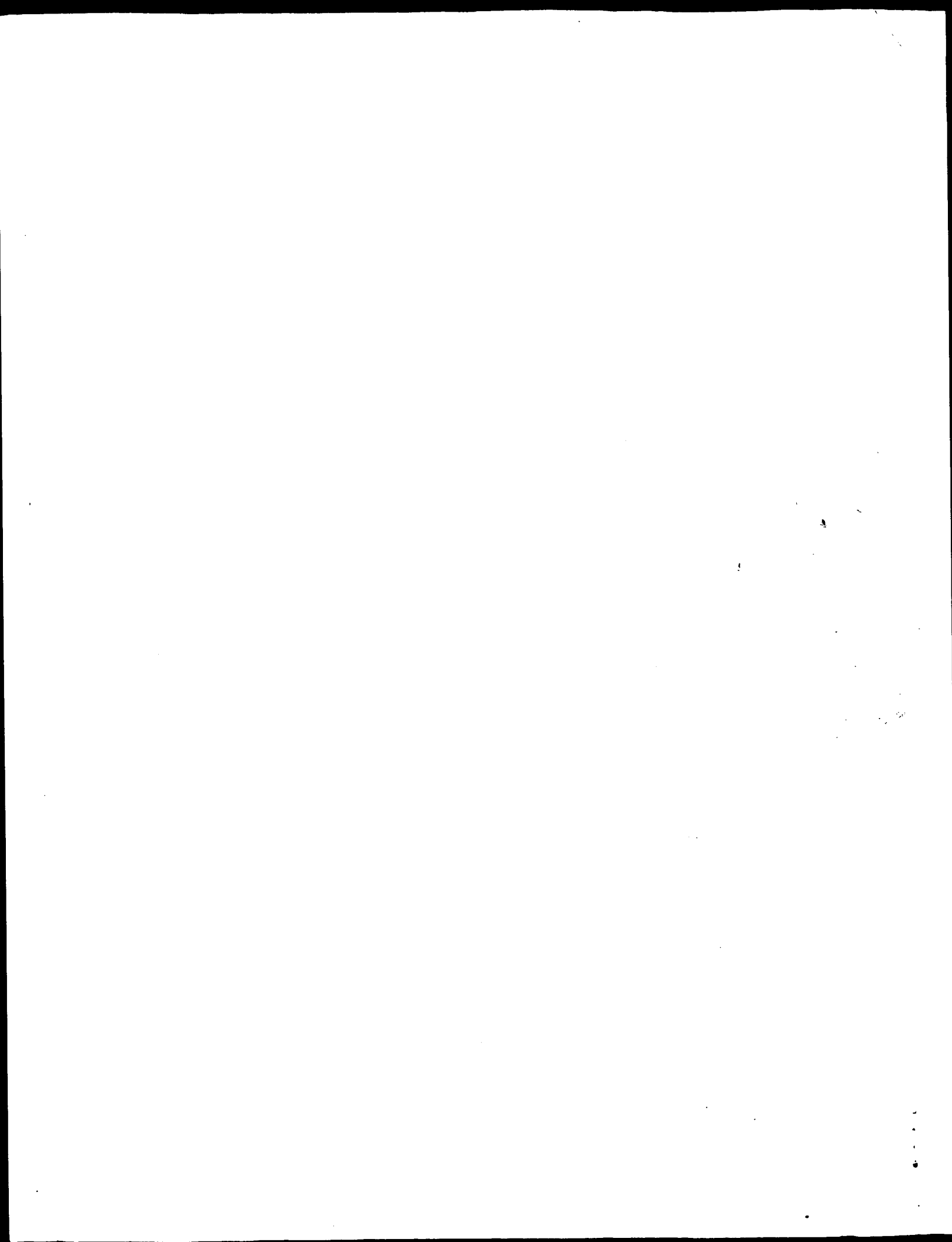
QY  2 EFHRWSSYM 10
    |||||
Db  548 EFHRWSSYM 556

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Search completed: September 13, 2000, 02:25:26
Job time: 169 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:23:37 ; Search time 17.58 Seconds
(without alignments)
49.283 Million cell updates/sec

Title: US-09-155-076-1

Perfect score: 14
Sequence: 1 AEFHRSSVYVHWK 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : PIR_64:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	583	2	acetylcholinestera
2	14	100.0	584	2	acetylcholinestera
3	14	100.0	614	2	acetylcholinestera
4	14	100.0	614	2	acetylcholinestera
5	14	100.0	614	2	acetylcholinestera
6	9	64.3	596	1	acetylcholinestera
7	9	64.3	599	1	acetylcholinestera
8	9	64.3	767	2	acetylcholinestera
9	6	42.9	330	2	DNA methyltransfer
10	6	42.9	469	2	probable Rieske ir
11	5	35.7	159	2	hypothetical prote
12	5	35.7	222	2	conserved hypotet
13	5	35.7	236	1	homeotic protein H
14	5	35.7	250	1	homeotic protein H
15	5	35.7	255	1	hypothetical prote
16	5	35.7	282	2	conserved hypotet
17	5	35.7	282	2	conserved hypotet
18	5	35.7	318	2	hypothetical prote
19	5	35.7	335	1	conserved hypotet
20	5	35.7	338	2	oxidoreductase - D
21	5	35.7	339	2	hypothetical prote
22	5	35.7	357	2	probable hemolysin
23	5	35.7	365	2	cysteine proteinase
24	5	35.7	408	2	hypothetical prote
25	5	35.7	415	2	probable acyl-CoA
26	5	35.7	428	2	S-locus-specific g
27	5	35.7	429	2	S-receptor kinase
28	5	35.7	431	2	S-locus-specific g
29	5	35.7	440	2	hypothetical prote

30 5 35.7 444 1 F69904
31 5 35.7 444 2 T11474
32 5 35.7 456 2 B65029
33 5 35.7 486 1 B41966
34 5 35.7 525 2 T34556
35 5 35.7 531 2 T39692
36 5 35.7 540 2 S76584
37 5 35.7 546 2 T46718
38 5 35.7 586 2 T19406
39 5 35.7 603 2 S70849
40 5 35.7 619 2 F81532
41 5 35.7 619 2 F72006
42 5 35.7 636 2 T38010
43 5 35.7 770 2 T07692
44 5 35.7 871 2 T43427
45 5 35.7 919 2 S28179

ALIGNMENTS

RESULT 1
SI0712
acetylcholinesterase (EC 3.1.1.7) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-Nov-1993 #sequence.revision 23-Mar-1995 #text_change 12-May-1995
C:Accession: SI0712; A39734; B39734; B25650
R:Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry,
FEBS Lett. 266, 123-127, 1990
A:Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and
A:Reference number: SI0712; MUID:90306335
A:Accession: SI0712
A:Molecule type: protein
A:Residues: 1-583 <DOC>
A:Experimental source: fetal serum
R:Roberts, W.D.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.
J. Biol. Chem. 266, 7481-7487, 1991
A:Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit
A:Reference number: A39734; MUID:91210255
A:Accession: A39734
A:Molecule type: protein
A:Residues: 1-15, R, 17-38; 225-235, X', 237-244; 248-264, X', 266-273; 365-380; 396-404, X'
A:Experimental source: brain, erythrocyte
A:Accession: B39734
A:Molecule type: protein
A:Residues: 1-38 <R02>
A:Experimental source: fetal serum
R:Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A:Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s
inesterase.
A:Reference number: A91370; MUID:87080761
A:Accession: B25650
A:Molecule type: protein
A:Residues: 'XS', 3-12 <BON>
A:Experimental source: caudate nucleus
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F;32-538/Domain: cholinesterase homology <CHE>
F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 14; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 8.9e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRSSVYVHWK 14

Db 555 AEFHRSSVYVHWK 568

RESULT 2

S48724
 acetylcholinesterase - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
 C:Accession: S48724
 R:Jbilo, O.; L'Hernite, Y.; Talses, V.; Toutant, J.P.; Chatonnet, A.
 Eur. J. Biochem. 225, 115-124, 1994
 A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissue
 A:Reference number: S48724; MUID:95010096
 A:Accession: S48724
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-584 <JBIL>
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: glycoprotein
 F:32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 584;
 Best Local Similarity 100.0%; Pred. No. 8.9e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||
 Db 556 AEFHRWSSYVHWK 569
 |||

RESULT 3
 JH0811
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Jun-1999
 C:Accession: JH0811
 R:Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
 J. Neurochem. 60, 337-346, 1993
 A:Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul
 A:Reference number: JH0811; MUID:93107932
 A:Accession: JH0811
 A:Molecule type: mRNA
 A:Residues: 1-614 <LEG>
 A:Cross-references: GB:S50879; NID:Q262092; PIDN:AAB24586.1; PID:Q262093
 A:Experimental source: striatum
 C:Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
 F:53-569/Domain: cholinesterase homology <CHE>
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted
 F:234,365,478/Active site: Ser, Glu, His #status predicted
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 14; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.2e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||
 Db 586 AEFHRWSSYVHWK 599
 |||

RESULT 4
 A39256
 acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
 C:Species: Homo sapiens (man)
 C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1999
 C:Accession: A39256; S03959
 R:Scorq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw
 Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
 A:Title: Molecular cloning and construction of the coding region for human acetylcholine
 A:Reference number: A39256; MUID:91088577
 A:Accession: A39256

A:Molecule type: mRNA; DNA
 A:Residues: 1-614 <SOR>
 A:Cross-references: GB:M5040; NID:g177974; PIDN:AAA68151.1; PID:g177975
 A:Note: this sequence represents composite of clones including clone ABGACHE from adu
 nce should represent an authentic brain splice form
 R:Chajlani, V.; Derr, D.; Earles, B.; Schmeil, E.; August, T.
 FEBS Lett. 247, 279-282, 1989
 A:Title: Purification and partial amino acid sequence analysis of human erythrocyte a
 A:Reference number: S03959; MUID:89232136
 A:Accession: S03959
 A:Molecule type: protein
 A:Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-3
 Y',532-551 <CHE>
 A:Experimental source: erythrocytes
 A:Note: this form was a disulfide-linked homodimer
 C:Genetics:
 A:Gene: GDB:ACHE; YT
 A:Cross-references: GDB:118746; OMIM:100740
 A:Map position: 7q22-7q22
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphati
 F:63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 14; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.2e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||
 Db 586 AEFHRWSSYVHWK 599
 |||

RESULT 5
 JH0314
 acetylcholinesterase (EC 3.1.1.7) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999
 C:Accession: JH0314
 R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
 Neuron 5, 317-327, 1990
 A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alte
 A:Reference number: JH0314; MUID:90380429
 A:Accession: JH0314
 A:Molecule type: mRNA
 A:Residues: 1-614 <RAC>
 A:Cross-references: EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845
 A:Experimental source: brain
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-614/Product: acetylcholinesterase #status predicted <MAT>
 F:63-569/Domain: cholinesterase homology <CHE>
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted
 F:234/Active site: Ser #status predicted
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 14; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 9.2e-10; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
 |||
 Db 586 AEFHRWSSYVHWK 599
 |||

RESULT 6
 AC9YE
 acetylcholinesterase (EC 3.1.1.7) precursor, 11S form - Pacific electric ray
 N:Alternate names: acetylcholinesterase, asymmetric form
 C:Species: Torpedo californica (Pacific electric ray)
 C>Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 26-Feb-1999

C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F
 Nature 319, 407-409, 1986
 A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
 A;Reference number: A00773; MUID:86118676
 A;Accession: A00773
 A;Molecule type: mRNA
 A;Residues: 557-596 <SCH>
 A;Cross-references: GB:X03439; NID:g64389
 A;Experimental source: electric organ
 A;Note: parts of this sequence, including the amino and carboxyl ends of the mature protein
 R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F
 Fed. Proc. 45, 2976-2981, 1986
 A;Title: Primary structure of acetylcholinesterase: implications for regulation and function
 A;Reference number: A60820; MUID:87054662
 A;Accession: A60820
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 22-596 <SC2>
 R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
 J. Biol. Chem. 263, 18979-18987, 1988
 A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylcholinesterase
 A;Reference number: A92701; MUID:89066695
 A;Accession: A31962
 A;Molecule type: mRNA
 A;Residues: 1-23 <SC3>
 A;Cross-references: EMBL:X03439; NID:g64389
 A;Experimental source: clones Ache-11 and Ache-18
 A;Note: revision to sequence A00773
 A;Accession: B31962
 A;Molecule type: DNA; mRNA
 A;Residues: 499-565 <SC4>
 A;Cross-references: GB:X03439; NID:g64389
 A;Experimental source: clone Ache-1
 R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
 J. Biol. Chem. 260, 12185-12189, 1985
 A;Title: Primary structures of the catalytic subunits from two molecular forms of acetylcholinesterase
 A;Reference number: A23902; MUID:86008285
 A;Accession: A23902
 A;Molecule type: protein
 A;Residues: 22, B, 24-45; 214-237 <MAC>
 A;Note: active site Ser identification
 R;Kreienkamp, H.J.; Weiss, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
 A;Reference number: A41117; MUID:91296772
 A;Accession: B41117
 A;Molecule type: protein
 A;Residues: 100-108 <KRE>
 A;Note: substrate binding site
 R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
 Neuron 4, 289-301, 1990
 A;Title: Single gene encodes glycopospholipid-anchored and asymmetric acetylcholinesterase
 A;Reference number: P50113; MUID:90166618
 A;Accession: S15677
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 557-596 <MAU>
 A;Cross-references: EMBL:X56516
 R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
 J. Biol. Chem. 261, 13565-13570, 1986
 A;Title: Profile of the disulfide bonds in acetylcholinesterase.
 A;Reference number: A43059; MUID:87008586
 A;Contents: annotation; disulfide bonds
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 submitted to the Brookhaven Protein Data Bank, October 1991
 A;Reference number: A50061; PDB:1ACE
 A;Contents: annotation: X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of
 R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Tokar, L.; Silman, I.
 Science 253, 872-879, 1991
 A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
 A;Reference number: A43098; MUID:91343928
 A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481, 511-555 of

C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with
 hollinesterase occurs on the outer surfaces of cell membranes, including those of eryt
 C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer
 C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology
 C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
 F:51-555/Domain: cholinesterase homology <CHE>
 F:80,478,554/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:88-115,275-286,423-542/Disulfide bonds: #status experimental
 F:105/Binding site: substrate (Trp) #status experimental
 F:221/Active site: Ser #status experimental
 F:348,461/Active site: Glu, His #status predicted
 F:437/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:593/Disulfide bonds: interchain #status experimental
 Query Match 64.3% Score 9; DB 1; Length 596;
 Best Local Similarity 100.0%; Pred. No. 0.00098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 EFHRWSSYM 10
 Db 569 EFHRWSSYM 577
 RESULT 7
 A38868
 acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
 C;Species: Torpedo marmorata (marbled electric ray)
 C;Date: 23-Apr-1993 #sequence.Revision 15-Nov-1996 #text_change 11-Jun-1999
 C;Accession: A38868; A29682; S15696; A25650
 R;Massoulié, J.; Bon, S.
 submitted to the EMBL Data Library, June 1992
 A;Reference number: A38868
 A;Accession: A38868
 A;Molecule type: mRNA
 A;Residues: 1-599 <MAS>
 A;Cross-references: EMBL:X05497; NID:g64414; PIDN:CAA29047.1; PID:g64415
 R;Sikorav, J.L.; Krejci, E.; Massoulié, J.
 EMBO J. 6, 1865-1873, 1987
 A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure
 A;Reference number: A29682; MUID:88004392
 A;Accession: A29682
 A;Molecule type: mRNA
 A;Residues: 1-40, 'G', 42-226, 'G', 228-272, 'G', 274-284, 'E', 286-420, 'N', 422-599 <SIK>
 A;Cross-references: EMBL:X05497
 R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund,
 EMBO J. 7, 2983-2993, 1988
 A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo
 A;Reference number: S01293; MUID:89030590
 A;Accession: S15696
 A;Molecule type: mRNA
 A;Residues: 526-599 <SI2>
 A;Cross-references: EMBL:X13172; NID:g64416; PIDN:CAA31570.1; PID:g64417
 A;Experimental source: clone pACHE2
 R;Bon, S.; Chang, J.X.; Strosberg, A.D.
 FEBS Lett. 209, 206-212, 1986
 A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-s
 inesterase.
 A;Reference number: A91370; MUID:87080761
 A;Accession: A25650
 A;Molecule type: protein
 A;Residues: 25-40, 'G', 42-47 <BON>
 C;Genetics:
 A;Gene: AChE
 C;Function:
 A;Description: hydrolyzes acetylcholine to choline and acetate
 A;Pathway: neurotransmitter degradation
 C;Superfamily: cholinesterase; cholinesterase homology

C:Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmitter
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-599/Product: acetylcholinesterase #status predicted <WAT>
 F:54-554/Domain: cholinesterase homology <CHE>
 F:83,440,481,557/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:91-118,278-289,426-545/Disulfide bonds: #status predicted
 F:224,351,464/Active site: Ser, Glu, His #status predicted
 F:596/Disulfide bonds: Interchain #status predicted

Query Match 64.3%; Score 9; DB 1; Length 599;
 Best Local Similarity 100.0%; Pred. No. 0.00099;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EPHRWSSYM 10
 |||||
 DB 572 EPHRWSSYM 580

RESULT 8

S47639
 Acetylcholinesterase (EC 3.1.1.7) - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
 C:Accession: S47639
 R:Randall, W.R.; Rimer, M.; Gough, N.R.
 Biochim. Biophys. Acta 1218, 453-456, 1994
 A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle and
 A:Reference number: S47639; MUID:94325359
 A:Accession: S47639
 A:Molecule type: mRNA
 A:Residues: 1-767 <RAN>
 A:Cross-references: EMBL:U03472; NID:G623031; PID:G424115
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase

Query Match 64.3%; Score 9; DB 2; Length 767;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EPHRWSSYM 10
 |||||
 DB 740 EPHRWSSYM 748

RESULT 9

S53990
 DNA methyltransferase pmt1 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2000
 C:Accession: S53990; T39793
 R:Wilkinson, C.R.M.; Bartlett, R.; Nurse, P.; Bird, A.P.
 Nucleic Acids Res. 23, 203-210, 1995
 A:Title: The fission yeast gene pmt1(+) encodes a DNA methyltransferase homologue.
 A:Reference number: S53990; MUID:95166638
 A:Accession: S53990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-330 <WIL>
 A:Cross-references: EMBL:X82444; NID:G563910; PIDN:CAA57824.1; PID:G563911
 R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 Submitted to the EMBL Data Library, July 1999
 A:Reference number: Z21880
 A:Accession: T39793
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-330 <MCD>
 A:Molecule type: DNA
 A:Cross-references: EMBL:AL109731; PIDN:CAB52029.1; GSPDB:GN000067; SPDB:SPBIC19C2.02
 A:Experimental source: strain 972h; cosmid c19C2
 C:Genetics:
 A:Gene: SPBIC19C2.02
 A:Map position: 2

A: Introns: 56/3
 C: Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII

Query Match 42.9%; Score 6; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYMW 11
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 DB 208 WSSYMW 213

RESULT 10

S74825
 probable Rieske iron-sulfur protein sir1747 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S74825
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
 S.

A:Reference number: S74322; MUID:97061201

A:Accession: S74825
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-469 <KAN>
 A:Cross-references: EMBL:D90909; GB:AB001339; NID:G1652844; PIDN:BAAL7786.1; PID:diol
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: Rieske [2Fe-2S] homology
 C:Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
 F:56-114/Domain: Rieske [2Fe-2S] homology <RSK>
 F:76,78,96,99/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status pr

Query Match 42.9%; Score 6; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRW 6
 |||||
 DB 349 AEFHRW 354

RESULT 11

H81442
 hypothetical protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11168)
 C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 C:Accession: H81442
 R:Parkhill, J.; Wren, B.W.; Muncall, K.; Kettle, J.M.; Churcher, C.; Basham, D.; Chil
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
 Nature 403, 665-668, 2000
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
 A:Reference number: AB1250; MUID:20150912
 A:Accession: H81442
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-159 <PAR>
 A:Cross-references: GB:AL139074; GB:AL111168; NID:G6967505; PIDN:CAB7217.1; PID:G696
 C:Experimental source: serotype O2, strain NCTC 11168
 C:Genetics:
 A:Gene: Cj0249

Query Match 35.7%; Score 5; DB 2; Length 159;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5

Db 20 AEFHR 24
|||||

RESULT 12

F81124 conserved hypothetical protein NMB1075 [imported] - Neisseria meningitidis (group B strain F81124)

C:Species: Neisseria meningitidis

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000

C:Accession: F81124

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.;

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755

A:Accession: F81124

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <TEXT>

A:Cross-references: GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF41470.1; PID:g722631

A:Experimental source: serogroup B, strain MMD58

C:Genetics:

A:Gene: NMB1075

Query Match

Best Local Similarity 35.7%; Score 5; DB 2; Length 222;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHR 5

|||||

Db 75 AEFHR 79

RESULT 13

S09256 homeotic protein Hox D4 - chicken

N:Alternate names: homeotic protein Chox-4.2; homeotic protein Chox-a

C:Species: Gallus gallus (chicken)

C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 24-Jul-1997

C:Accession: S09256

R:Sasaki, H.; Yokoyama, E.; Kuroiwa, A.

Nucleic Acids Res. 18, 1739-1747, 1990

A>Title: Specific DNA binding of the two chicken deformed family homeodomain proteins, c

A:Reference number: S09256; MUID:90245562

A:Accession: S09256

A:Molecule type: mRNA

A:Residues: 1-236 <SAS>

A:Cross-references: EMBL:X52671; EMBL:X52672

C:Genetics:

A:Gene: hoxd-4

C:Function:

A:Description: control of embryonic development by tissue- and stage-specific regulation

C:Superfamily: homeotic protein Hox D4; homeobox homology

C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

F:146-202/Domain: homeobox homology <Hox>

Query Match

Best Local Similarity 35.7%; Score 5; DB 1; Length 236;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11

|||||

Db 4 SSYMV 8

RESULT 14

A36170 homeotic protein Hox D4 - mouse

N:Alternate names: homeotic protein Hox 4.2; homeotic protein Hox 5.1

C:Species: Mus musculus (house mouse)

C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jul-1997

C:Accession: A36170

R:Featherstone, M.S.; Baron, A.; Gaunt, S.J.; Mattei, M.G.; Duboule, D.

Proc. Natl. Acad. Sci. U.S.A. 85, 4760-4764, 1988

A>Title: Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome 2.

A:Reference number: A36170; MUID:88263027

A:Accession: A36170

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-250 <FEA>

A:Cross-references: GB:J03770

C:Genetics:

A:Gene: Hoxd-4

A:Map position: 2

C:Function:

A:Description: control of embryonic development by tissue- and stage-specific regulat

C:Superfamily: homeotic protein Hox D4; homeobox homology

C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

F:153-209/Domain: homeobox homology <Hox>

Query Match

Best Local Similarity 35.7%; Score 5; DB 1; Length 250;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYMV 11

|||||

Db 4 SSYMV 8

RESULT 15

WJHU4B

homeotic protein Hox D4 - human

N:Alternate names: homeotic protein c13; homeotic protein Hox 4B; homeotic protein Ho

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999

C:Accession: S10985; A38787; A25238; S15546

R:Cianetti, L.; di Cristofaro, A.; Zappavigna, V.; Bottero, L.; Boccoli, G.; Testa, U

Nucleic Acids Res. 18, 4361-4368, 1990

A>Title: Molecular mechanisms underlying the expression of the human HOX-5.1 gene.

A:Reference number: S10985; MUID:90356367

A:Accession: S10985

A:Molecule type: DNA

A:Residues: 1-255 <CIA>

A:Cross-references: EMBL:X17360; NID:g32394; PIDN:CAA35237.1; PID:g296652

A:Accession: A38787

A:Molecule type: mRNA

A:Residues: 1-122,'S',124-255 <CIA2>

R:Navilio, F.; Simeone, A.; Giampaolo, A.; Faiella, A.; Zappavigna, V.; Acampora, D.;

Nature 324, 664-668, 1986

A>Title: Differential and stage-related expression in embryonic tissues of a new huma

A:Reference number: A25238; MUID:87090377

A:Accession: A25238

A:Molecule type: mRNA

A:Residues: 1-122,'S',124-141,'A',143-255 <MAV>

A:Cross-references: EMBL:X04706; NID:g32366; PIDN:CAA28411.1; PID:g32367

R:Bocchini, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.;

Genome 31, 745-756, 1989

A>Title: Organization of human class I homeobox genes.

A:Reference number: S15036; MUID:90215256

A:Accession: S15036

A:Molecule type: DNA

A:Residues: 154-219 <BON>

C:Genetics:

A:Gene: GDB:HOXD4

A:Cross-references: GDB:120677; OMIM:142981

A:Map position: 2q31-2q31

A:Introns: 145/1

C:Function:

A:Description: control of embryonic development by tissue- and stage-specific regulat

C:Superfamily: homeotic protein Hox D4; homeobox homology

C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

F:155-211/Domain: homeobox homology <HOX>

Query Match 35.7%; Score 5; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SSYMW 11
 |||||
Db 4 SSYMW 8

Search completed: September 13, 2000, 02:25:55
Job time: 138 sec

OM of: US-09-155-076-1 to: GenEmbl.* out_format : pfs

Date: Sep 13, 2000 3:47 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
-MODEL=frame+pin.model -DEV=xlp
-O=/cgn2.1/USPTO_spool/US09155076/runat_29082000_092538_16909/app_query.fasta_1.144
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-GAPEXT=0.050 -GAPOP=6.000 -GAPEXT=60.000 -GAPOP=6.000
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-DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15
-MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000
-USER=US09155076_ECGN1_1_3119 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
-WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: GenEmbl.*

Database sequences: 972840

Database length: 892348106

Search time (sec): 760.820000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000

WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

Seqname	Strd Orig	Zscore	Escore	Len	Documentation
gb_om:BTACHE4	+	14.00	305.02	140	AF061816 Bos taurus acetylcholinesterase
gb_pr3:HUMACHE04	+	14.00	296.89	147	L22562 Human acetylcholinesterase
gb_om:OCU05036	+	14.00	287.51	1947	U05036 Oryctolagus cuniculus acetylcholinesterase
gb_ro:S50879	+	14.00	287.11	2066	S50879 acetylcholinesterase T
gb_ro:HWACHE	+	14.00	287.04	2089	X56518 Mouse mRNA for acetylcholinesterase
gb_pr2:HUMACHE	+	14.00	286.64	2218	M5040 Human acetylcholinesterase
gb_pat:AR070205	+	14.00	286.53	2236	AR070205 Sequence 5 from patent
gb_pat:AR070207	+	14.00	284.60	3016	AR070207 Sequence 7 from patent
gb_pat:AR070206	+	14.00	284.42	3096	AR070206 Sequence 6 from patent
gb_om:AF053485	+	14.00	282.79	3958	AF053485 Felis catus acetylcholinesterase
gb_pr3:HUMACHEB	+	14.00	282.42	4195	L42812 Homo sapiens acetylcholinesterase
gb_pr3:HSFA002993	+	14.00	268.31	34221	AF002993 Homo sapiens cosmid
gb_htg29:AC011895	-	14.00	257.58	175155	AC011895 Homo sapiens chromosome
gb_ov:AF030422	+	10.00	196.67	4472	AF030422 Electrophorus electricus
gb_ov:TMACHE2	+	9.00	188.65	605	X13172 Torpedo marmorata mRNA
gb_ov:TCACHE3A	+	9.00	180.34	2110	X56516 Torpedo marmorata acetylcholinesterase
gb_ov:TMACHE	+	9.00	179.40	2357	X05497 Torpedo marmorata mRNA
gb_ov:TCACER	+	9.00	179.24	2490	X03439 Torpedo californica mRNA
gb_ov:GGU03472	+	9.00	175.25	4536	U03472 Gallus gallus acetylcholinesterase
gb_pl3:AF220204	-	7.00	136.90	1577	AF220204 Malus domestica unknown
gb_in2:CEUK04F1	-	7.00	109.14	42613	AF106575 Caenorhabditis elegans
gb_htg13:AC021287	+	7.00	117.70	154385	AC021287 Homo sapiens clone
gb_htg18:AC024535	+	7.00	108.96	158463	AC024535 Homo sapiens chromosome
gb_ov:AC023535	+	7.00	108.80	162434	AC023535 Homo sapiens chromosome
gb_htg18:AC024043	+	7.00	108.45	606.21	171247 Homo sapiens chromosome
gb_ov:AC021842	+	7.00	107.83	187956	AC021842 Homo sapiens chromosome
gb_vil:MLMTGA	+	6.00	137.41	14.76	M12274 Moloney murine leukemia virus
gb_pr2:HS285900	+	6.00	130.65	35.14	285900 H.sapiens BF2p3-Kg3-B08
gb_pr2:S63199	+	6.00	130.26	36.96	S63199 Ig kappa V3 [human, chimeric]
gb_vil:FIVSEQ	+	6.00	127.05	55.79	L16939 Feline immunodeficiency virus
gb_in2:G23571	-	6.00	126.68	58.48	G23571 human STS WI-14862, sequence
gb_in1:AF033946	+	6.00	125.10	71.63	AF033946 Bactrocera quadriseta
gb_sts:CSN01HKO	+	6.00	125.04	72.17	AL144555 Anopheles gambiae STS
gb_pr3:HS079588	+	6.00	125.02	72.39	U79588 Human clone OR immunoglobulin
gb_sts:CSN01OR9	+	6.00	123.99	82.59	AL153877 Anopheles gambiae STS
gb_pr2:CSN01A5J	+	6.00	123.51	87.82	AL125111 Botrytis cinerea STS
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gb_htg31:AC066684	-	6.00	123.00	93.72	AC066684 Giardia intestinalis
gb_htg30:AC064060	+	6.00	122.41	101.08	AC064060 Giardia intestinalis

gb_ro:AF139769 + 6.00 122.36 101.79 856 AF139769 Mus musculus type 1
gb_htg28:AC059401 + 6.00 121.70 110.75 945 AC059401 Giardia intestinalis
gb_sts:CSN01M4L - 6.00 121.55 112.95 967 AL150470 Anopheles gambiae STS
gb_pl2:AU035826 - 6.00 121.32 116.33 1001 U35826 Arabidopsis thaliana
gb_htg28:AC056188 + 6.00 121.24 117.51 1013 AC056188 Giardia intestinalis
gb_in1:DME271414 - 6.00 120.89 122.93 1068 AJ271414 Drosophila melanogaster

seq_name: gb_om:BTACHE4

seq_documentation_block: 140 bp DNA 16-OCT-1998
LOCUS BTACHE4
DEFINITION Bos taurus acetylcholinesterase T-subunit precursor (Ache) gene,
exon 6 and partial cds.

ACCESSION AF061816

VERSION AF061816.1 GI:3746574

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Bos taurus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

REFERENCE

AUTHORS

TITLE

Characterization

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

Direct Submission

JOURNAL

Submitted (28-APR-1998) Biochemistry and Molecular Genetics, Israel

Institute for Biological Research, PO Box 19, Ness Ziona 70450,

Israel

FEATURES

Location/Qualifiers

1..140

/organism="Bos taurus"

/db_xref="taxon:9913"

/dev_stage="adult"

/sex="male"

/tissue_type="kidney"

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AF061815.1:1..188.1.>127)

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exon

/gene="Ache"

/number=6

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/product="acetylcholinesterase T-subunit precursor"

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/function="cholinesterase"

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BASE COUNT 32 a 39 c 47 g 22 t

ORIGIN

alignment_scores:

Quality: 14.00 Length: 14

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x BTACHE4

Align seg 1/1 to: BTACHE4 from: 1 to: 140

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14

|||||
42 GCGAGTTCATCGCTGGAGCTCCCTACATGCTGCTGGAAG 83

seq_name: gb_pr3:HUMACHE04

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LOCUS HUMACHE04 475 bp DNA PRI 14-JUN-1995
DEFINITION Human acetylcholinesterase (ACHE) gene, exon 6.
ACCESSION L22562
VERSION L22562.1 GI:862302
KEYWORDS acetylcholinesterase.
SEGMENT 4 of 4
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,
Neville,L., Lieman-Hurwitz,J., Lev-Lehman,E., Ginzberg,D.,
Lapidot-Lifson,Y. and Zakut,H.
TITLE Molecular cloning and construction of the coding region for human
acetylcholinesterase reveals a G + C-rich attenuating structure
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)
MEDLINE 91088577
REFERENCE 2 (sites)
AUTHORS Li,Y., Camp,S., Rachinsky,T.L., Getman,D. and Taylor,P.
TITLE Gene structure of mammalian acetylcholinesterase. Alternative exons
dictate tissue-specific expression
J. Biol. Chem. 266 (34), 23083-23090 (1991)
MEDLINE 92078174
REFERENCE 3 (bases 1 to 475)
AUTHORS Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for YF blood group polymorphism
Am. J. Hum. Genet. 52 (5), 928-936 (1993)
JOURNAL 93256075
MEDLINE
COMMENT On Jun 15, 1995 this sequence version replaced gi:857448.
**Reference [1] reports bases 142-480;
Reference [J. Biol. Chem. 266, 23083-23090 (1991)] reports bases
132-141.
Reference [3] reports bases 1-131**.
FEATURES
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-155-076-1 x HUMACHE04 ..

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169 GCGAGTTCACCGCTGGAGCTCCTACATGCTGCTGGAAG 210

seq_name: gb_om:OCU05036

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seq_documentation_block:
LOCUS OCU05036 1947 bp mRNA MAM 28-NOV-1994
DEFINITION Oryctolagus cuniculus acetylcholinesterase mRNA, partial cds.
ACCESSION U05036
VERSION U05036.1 GI:576446
KEYWORDS
SOURCE Oryctolagus cuniculus.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1947)
AUTHORS Jbilo,O., Ihermite,Y., Toutant,J. and Chatonnet,A.
TITLE Acetylcholinesterase and Butyrylcholinesterase expression in adult
rabbit tissues and during development
Eur. J. Biochem. 225, 115-124 (1994)
JOURNAL 95010096
MEDLINE
REFERENCE 2 (bases 1 to 1947)
AUTHORS Chatonnet,A.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-1994) Arnaud Chatonnet, Physiologie Animale,
Institut National de la Recherche Agronomique, Place Viala,
Montpellier, 34060 France
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CLPSEAPGNGLLQRLALQWQENVAAGDPASVTLFGESAGAAVGLHLSPP
SRGLFRAVLQSGAPNPAWVGARRATLLARLVCPGAGGNDTELVACLRT
RPAQDLVDHEWRVLPQESIFRFSVPVWDGDFLSDPEALINAGDFQGLVGVYKD
EGYFLVYGAPGSKONESIFSAQFLAGVRCVQASDLAAFAVLHYTDLHPEDP
ARLDALSDVVGHNVCVPAQAGRLAQAQARVAYVFEHRASLTSLWFLMGVPHGY
EIEFIFGLPLEPSLNTTEERIFAQLRMRYWANFARTGDPNEPRDAPQWPPYTAGA
QQVYSLNRLPELVRRGLRAQACAFWRFLPKLLSATDTLDEAFERQWKAEFHRWSSYMW
HWKNQFDHYSKQDRCSDL"
BASE COUNT 299 a 655 c 560 g 333 t
ORIGIN

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alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x OCU05036 ..

Align seg 1/1 to: OCU05036 from: 1 to: 1947

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14

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1666 GCGAGTTCACCGCTGGAGCTCCTACATGCTGCTGGAAG 1707

seq_name: gb_ro:S50879

seq_documentation_block:


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LOCUS       S50879             2066 bp      mRNA           ROD           08-MAY-1993
DEFINITION   acetylcholinesterase T subunit [rats, mRNA Partial, 2066 nt].
ACCESSION    S50879
VERSION      S50879.1  GI:262092
KEYWORDS     Rattus sp.
SOURCE       Rattus sp.
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
              Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE    1 (bases 1 to 2066)
AUTHORS      Legay,C., Bon,S., Vernier,P., Coussen,F. and Massoulié,J.
TITLE        Cloning and expression of a rat acetylcholinesterase subunit:
              generation of multiple molecular forms and complementarity with a
              Torpedo collagenic subunit
JOURNAL       J. Neurochem. 60 (1), 337-346 (1993)
MEDLINE      93107932
REMARK       GenBank staff at the National Library of Medicine created this
              entry [NCBI gbbseq 121005] from the original journal article.
              This sequence comes from Fig. 1.
FEATURES     Location/Qualifiers
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                1..2066
                /organism="Rattus sp."
                /db_xref="taxon:10118"
              gene
                1..1845
                /gene="acetylcholinesterase T subunit, AChE"
              CDS
                1..1845
                /note="this sequence comes from Fig. 1; AChE"
                /codon_start=1
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                /protein_id="AAB24586.1"
                /db_xref="GI:262093"
              translation="MRPPWYPLHTPSLAPFLLLSLGGGARAEGREDPOLLAVRV
              GGOLGIRLKAPGPGVSAFLGIPRAEPVGSRRPEPKRPWSGLDATTQNVCYQ
              YVDLYPFGFEGTEMNPNRELSLCLINWVTPRTSPVLIWYGGFTSGASS
              LDVIDGRFLAQVEGAVLVSMNYRVGTGFLALPGSREAPGVNGLDQLRALQWQENI
              AAFGDPMSVTLFGESAGASVGMHILSPRSLSFRAVLQSGTPNGPWATVSAGEAR
              RRATLLARLVGCPGGAGNDTELSCLTRPAQDLVDHEWHLVQESIFRFSFPVY
              DGFLLSDPTDGLQDFQDLQVLGVVKGDSYFLVGVGFKDNESLISRAQFLA
              GVRIGVPOASDLAAEAVALVHTDMLHPEDPAHLRDAMSADVGDHNVVCPVAQLAGRLA
              AGARVAYIFEHRASTLTWPLWGVPHGIEIEIFGLDPLDSLVNYVERIFAQRLM
              QYWNFARTGDPNDPRDSKSPWPPTTAAQYVSLNKLPLEVRARGURATCAFNNRF
              LPKLLSATDITLDEAEKQWKAEFHRSWSSYMHVKNQFDHYSKQERCSDL"
              BASE COUNT      394 a 629 c 590 g 453 t
              ORIGIN

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
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  Align seg 1/1 to: S50879 from: 1 to: 2066

1 AlaGluPheHisArgTrrpSerTyrMetValHisTriPlys 14
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1756 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCTGGAAG 1797

seq_name: gb_ro:MMACHE

seq_documentation_block:
LOCUS       MMACHE             2089 bp      mRNA           ROD           20-JUL-1995
DEFINITION   Mouse mRNA for acetylcholinesterase.
ACCESSION    X56518
VERSION      X56518.1  GI:49844
KEYWORDS     acetylcholinesterase.
SOURCE       house mouse.
ORGANISM     Mus musculus
              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
              Rodentia; Sciurognathi; Muridae; Murinae; Mus.

LOCUS       S50879             2089 bp      mRNA           PRI           09-JUN-1995
DEFINITION   Human acetylcholinesterase (ACHE) mRNA, complete cds.
ACCESSION    M55040
VERSION      M55040.1  GI:177974
KEYWORDS     acetylcholinesterase.
SOURCE       Human 21-week old fetus DNA, and cDNA to mRNA.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
              Eutheria; Primates; Catarrhini; Hominiidae; Homo.
              Soreq,H.E., Ben-Aziz,R., Prody,C.A., Seidman,S., Gnatt,A.,

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Neville, L., Lieman-Hurwitz, J., Lev-Lehman, E., Ginzberg, D.,
Lapidot-Lifson, I., and Zukut, H.
Molecular cloning and construction of the coding region for human
acetylcholinesterase reveals a G + C-rich attenuating structure
Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9688-9692 (1990)
91088577 Location/Qualifiers
source
1..2218
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="21-week-old fetus"
/tissue_lib="lambda-gt10"
/map="7q22"
1..2218
/gene="ACHE"
/note="G00-118-746"
/product="acetylcholinesterase"
1..2218
/gene="ACHE"
157..2001
/gene="ACHE"
/EC_number="3.1.1.7"
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/db_xref="GDB:G00-118-746"
/product="acetylcholinesterase"
/protein_id="AA68151.1"
/db_xref="GI:177975"
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LDVYDRLVQARTVLSVMNYRVGAFGLALPGREAPGNVGLLQRLALQWQENV
AAGGDDPTSVTLFESGAASVGMHLLSPSPRGLFRAVLQSGAPNGPWTGMEAR
BRATQLAHLVCCPGGTGGNDTELVAQLRTPAQVLVHEWHLVPOESVFERFVPV
DGDFLTPERALINAGDFHGLQVLGVYKDEGSFLVYAGPSSKONESLISRAEFLA
GVRGVPOVQDLAAEAVLHVDLWHPEDPARLEALSVDVGHNVVCPVQAQAGRLA
AQGARVAYVFEHRASTLSPLWMPVPHGYEIEIFIGIPLDPRNRYAEKIFAQRLM
RYWANFARTPGPPKAPQWPYPYGAQQYVSLDLRELVRRGLRAQACAFWNR
LPKLLSATDTLDEAERQWKAEFHRSWSSVMVHKNQFDHYSKQDRCSDL"
229..291
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/note="G00-118-746; does not fit consensus"
310..1998
/gene="ACHE"
/EC_number="3.1.1.7"
/note="G00-118-746"
/product="acetylcholinesterase"
BASE COUNT 355 a 755 c 580 g 428 t
ORIGIN

sig_peptide
229..291
/gene="ACHE"
/note="G00-118-746; does not fit consensus"
310..1998
/gene="ACHE"
/EC_number="3.1.1.7"
/note="G00-118-746"
/product="acetylcholinesterase"
BASE COUNT 355 a 755 c 580 g 428 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x HUMACHE ..
Align seg 1/1 to: HUMACHE from: 1 to: 2218

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1912 GCCGAGTTCCACCGCTGAGCTCTACATGTCGTCACCTGGAAG 1953

seq_name: gb_pat:AR070205

seq_documentation_block:
LOCUS AR070205 2256 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5891725.
ACCESSION AR070205
VERSION AR070205.1 GI:7221093
KEYWORDS Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2256)
AUTHORS Soreq, H., Zukut, H. and Eckstein, F.
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical
compositions containing them
JOURNAL Patent: US 5891725-A 5 06-APR-1999;
FEATURES Location/Qualifiers
source
1..2256
/organism="unknown"
BASE COUNT 390 a 757 c 580 g 429 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AR070205 ..
Align seg 1/1 to: AR070205 from: 1 to: 2256

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
1915 GCCGAGTTCCACCGCTGAGCTCTACATGTCGTCACCTGGAAG 1956

seq_name: gb_pat:AR070207

seq_documentation_block:
LOCUS AR070207 3016 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 7 from patent US 5891725.
ACCESSION AR070207
VERSION AR070207.1 GI:7221095
KEYWORDS Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3016)
AUTHORS Soreq, H., Zukut, H. and Eckstein, F.
TITLE Synthetic antisense oligodeoxynucleotides and pharmaceutical
compositions containing them
JOURNAL Patent: US 5891725-A 7 06-APR-1999;
FEATURES Location/Qualifiers
source
1..3016
/organism="unknown"
BASE COUNT 497 a 1065 c 840 g 614 t
ORIGIN

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x AR070207 ..
Align seg 1/1 to: AR070207 from: 1 to: 3016

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
2675 GCCGAGTTCCACCGCTGAGCTCTACATGTCGTCACCTGGAAG 2716

seq_name: gb_pat:AR070206

seq_documentation_block:
LOCUS AR070206 3096 bp DNA PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5891725.
ACCESSION AR070206
VERSION AR070206.1 GI:7221094
KEYWORDS Unknown.

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 3096)
AUTHORS      Soreq,H., Zakut,H. and Eckstein,F.
TITLE        Synthetic antisense oligodeoxynucleotides and pharmaceutical
              compositions containing them
JOURNAL      Patent: US 5891725-A 6 06-APR-1999;
FEATURES     Location/Qualifiers
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                1..3096
                /organism="unknown"
BASE COUNT   509 a 1089 c 872 g 626 t
ORIGIN
alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
  US-09-155-076-1 x AR070206 ..
  Align seg 1/1 to: AR070206 from: 1 to: 3096
1 AlagluPheHisArgTyrSerTyrMetValHisTriPlys 14
|||||
2755 GCGAGTCCACCGCTGGAGCTCTACATGGTGCACTGGAAG 2796

seq_name: gb_om:AF053485
seq_documentation_block:
LOCUS      AF053485      3958 bp      DNA      MAM      01-APR-1998
DEFINITION Felis catus acetylcholinesterase glycopospholipid-anchored form
            precursor (ACHE) and acetylcholinesterase collagen-tailed or
            globular form precursor (ACHE) genes, complete cds.
ACCESSION   AF053485
VERSION     AF053485.1 GI:3003019
KEYWORDS    cat.
SOURCE      Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1 (bases 1 to 3958)
AUTHORS     Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE       Sequence and characterization of domestic cat acetylcholinesterase
            and butyrylcholinesterase
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 3958)
AUTHORS     Bartels,C.F., Xie,W.-H., Miller-Lindholm,A.K. and Lockridge,O.
TITLE       Direct Submission
JOURNAL     Submitted (12-MAR-1998) Eppley Institute, University of Nebraska
            Medical Center, 600 S. 42nd St., Omaha, NE 68198-6805, USA
FEATURES     Location/Qualifiers
              source
                1..3958
                /organism="Felis catus"
                /db_xref="taxon:9685"
                join(<92..1150,1517..2001,2768..2937,3785..>3906)
                /product="acetylcholinesterase collagen-tailed or globular
                form precursor"
                join(<92..1150,1517..2001,2768..2937,3051..>3178)
                /gene="ACHE"
                /product="acetylcholinesterase glycopospholipid-anchored
                form precursor"
                join(92..1150,1517..2001,2768..2937,3051..3178)
                /gene="ACHE"
                /note="ACHE h-form; encoded by exon 4 spliced to exon 5"
                /codon_start=1
                /product="acetylcholinesterase glycopospholipid-anchored
                form precursor"

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/protein_id="AAC08996.1"
/db_xref="GI:3003021"
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YDRFLAQAGETVLVSNRYVGFALPGSREAPGNVGLLDQRLALQVQDNVATF
GGDPMSVTLFGESAGAAVGMHLLSPSRGLFRAVLQSGAPNGWATVGVGEARRRA
TLARLVGCPGGAGNDTELACLRTPAQDLVDHEWHVLPQESVFRFVPVVDGD
FLSDTPALINAGDFHGLQVLGVVKGDEGSYFLVYGAPGSKNESLISRAQFLAGVR
VGYQASDLAAEAVLHYTDWLPEDPARLREMSDVVGDHNVVCPVAQLAGRLAAG
ARVAYIFHRHASTLSWPLMWVPHGEIEIFGLPLEPSLNTYAEERIFAQRLMRYW
ANFARTGDPNDPRDPKVPQWPPYTAGAQYVSLDLPLEYVRGLRAQACAFWNRFLPK
LLSATASKAPSTCGSPAHGEAPRPGELSLPLILLLLLSRLRLR"
join(92..1150,1517..2001,2768..2937,3785..3906)
/gene="ACHE"
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/codon_start=1
/product="acetylcholinesterase collagen-tailed or globular
form precursor"
/protein_id="AAC08995.1"
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YDRFLAQAGETVLVSNRYVGFALPGSREAPGNVGLLDQRLALQVQDNVATF
GGDPMSVTLFGESAGAAVGMHLLSPSRGLFRAVLQSGAPNGWATVGVGEARRRA
TLARLVGCPGGAGNDTELACLRTPAQDLVDHEWHVLPQESVFRFVPVVDGD
FLSDTPALINAGDFHGLQVLGVVKGDEGSYFLVYGAPGSKNESLISRAQFLAGVR
VGYQASDLAAEAVLHYTDWLPEDPARLREMSDVVGDHNVVCPVAQLAGRLAAG
ARVAYIFHRHASTLSWPLMWVPHGEIEIFGLPLEPSLNTYAEERIFAQRLMRYW
ANFARTGDPNDPRDPKVPQWPPYTAGAQYVSLDLPLEYVRGLRAQACAFWNRFLPK
LLSATDTLDEAERQWKAEEFHRSSVMVHWKQDFHYSKQDRCSDL"
BASE COUNT 723 a 1256 c 1205 g 772 t 2 others
ORIGIN
alignment_scores:
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  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
  US-09-155-076-1 x AF053485 ..
  Align seg 1/1 to: AF053485 from: 1 to: 3958
1 AlagluPheHisArgTyrSerTyrMetValHisTriPlys 14
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3817 GCAGAGTCCACCGCTGGAGCTCTACATGGTGCACTGGAAG 3858

seq_name: gb_pr3:HUMACHEB
seq_documentation_block:
LOCUS      HUMACHEB      4185 bp      DNA      PRI      23-JUN-1995
DEFINITION Homo sapiens acetylcholinesterase (ACHE) gene, exons 2-6.
ACCESSION   L42812
VERSION     L42812.1 GI:854682
KEYWORDS    acetylcholinesterase.
SOURCE      Homo sapiens DNA.
            ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS     Bartels,C.F., Zelinski,T. and Lockridge,O.
TITLE       Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
            accounts for YF blood group polymorphism
JOURNAL     Am. J. Hum. Genet. 52 (5), 928-936 (1993)
REFERENCE   2 (bases 1 to 4185)
AUTHORS     Bartels,C.F., Morlearty,P.L., Becker,R.E., Robbs,R.S.,
            Sorenson,R.C., Mountjoy,C.P. and Lockridge,O.
TITLE       Polymorphic sites in the acetylcholinesterase gene of patients with
            Alzheimer's disease

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JOURNAL Unpublished (1995)
 FEATURES Location/Qualifiers
 source 1..4185
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 exon 75..1162
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 /note="G00-118-746"
 /number=2
 /evidence=experimental
 gene 75..4185
 /gene="ACHE"
 variation 1151
 /gene="ACHE"
 /note="Yr blood group; His322/Asn"
 /replace="a"
 intron 1163..1508
 /gene="ACHE"
 /note="G00-118-746"
 /number=3
 /evidence=experimental
 variation 1871
 /gene="ACHE"
 /note="Pro446/Pro"
 /replace="t"
 intron 1994..2988
 /gene="ACHE"
 /note="G00-118-746"
 /number=3
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 variation 2309
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 /note="G00-118-746"
 /number=4
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 /number=4
 /evidence=experimental
 exon 3239..3991
 /gene="ACHE"
 /note="includes retained intron 5; G00-118-746"
 /number=5
 /evidence=experimental
 variation 3290
 /gene="ACHE"
 /note="Pro 561 more common; C/G polymorphism at 3290; Pro561(CGG) or Arg 561(CGG)"
 /replace="g"
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 /note="G00-118-746"
 /number=6
 /evidence=experimental
 BASE COUNT 792 a 1320 c 1236 g 837 t
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Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
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 US-09-155-076-1 x HUMACHEB ..
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 1 AlaGluPheHisArgTyrSerTyrMetValHisTyrPls 14
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 4024 GCCGAGTTCCACCGTGGAGCTCTACATGCTGCTGGAAG 4065
 seq_name: gb_pr3:HSAF002993
 seq_documentation_block:
 LOCUS HSAF002993 34921 bp DNA PRI 01-JAN-1998
 DEFINITION Homo sapiens cosmid from 7q22, complete sequence.
 ACCESSION AF002993
 VERSION AF002993.1 GI:2735699
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 34921)
 AUTHORS Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.
 TITLE Genomic sequencing in 7q22 revealed a novel arsenite resistance gene
 JOURNAL Unpublished (1997)
 REFERENCE 2 (bases 1 to 34921)
 AUTHORS Drescher,B., Rosenthal,A., Hinzmann,B. and Korner,M.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

Location/Qualifiers
 1..34921
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 /evidence=not_experimental
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 /note="Region: Data base match"
 /evidence=not_experimental
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 exon 1474..1572
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 exon 1474..1572
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 exon 1657..1774
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 exon 1657..1774
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 exon 1947..2104
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 exon 1947..2104

alignment_scores:
 Quality: 14.00 Length: 14

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2105. .2434
/note="Alignment: EST, | Intron"
/evidence-not_experimental
2497. .2596
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2597. .2675
/note="M2EF, score = 98.9%"
/evidence-not_experimental
2676. .2980
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/evidence-not_experimental
3170. .3528
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/evidence-not_experimental
3529. .3585
/note="M2EF, score = 100%"
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3539. .3764
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/evidence-not_experimental
3548. .3702
/note="Xpound exon prediction, score = 98% (0%)"
/evidence-not_experimental
3637. .3702
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3703. .3780
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3781. .3934
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3781. .3934
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3781. .3927
/note="Alignment: CDS, |CG415001|85.7|112|258"
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Cricetulus griseus arsenite-resistance protein (ars2)
mRNA."
/note="Region: Data base match"
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4054. .4247
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/evidence-not_experimental
4191. .4220
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Cricetulus griseus arsenite-resistance protein (ars2)"
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4248. .4436
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4437. .4593
/note="M2EF, score = 97%"
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4437. .4593
/note="Xpound exon prediction, score = 89% (0%)"
/evidence-not_experimental
4437. .4593
/note="Alignment: CDS, |CG415001|86.6|457|613"
/evidence-not_experimental
4466. .4626
/note="BLASTN (EMBL), 453. .613 of emb|U41500|CG41500
Cricetulus griseus arsenite-resistance protein (ars2)
mRNA."
/note="Region: Data base match"
/evidence-not_experimental
4467. .4519
/note="BLASTX (GENPEPT), 87. .139 of gb|U41500|CG41500_1
Cricetulus griseus arsenite-resistance protein (ars2)"
/evidence-not_experimental
4594. .4788
/note="Alignment: EST, | Intron"
/evidence-not_experimental
4809. .4840
/note="BLASTX (GENPEPT), 140. .171 of gb|U41500|CG41500_1
Cricetulus griseus arsenite-resistance protein (ars2)"
/evidence-not_experimental
4879. .4991
/note="Alignment: CDS, | Intron"
/evidence-not_experimental
4992. .5118
/note="Alignment: CDS,
|CG415001|88.3|717|844|CG415002|88.6|1|44"
/evidence-not_experimental
5045. .5152
/note="BLASTN (EMBL), 738. .845 of emb|U41500|CG41500
Cricetulus griseus arsenite-resistance protein (ars2)
mRNA."
/note="Region: Data base match"
/evidence-not_experimental
5119. .5208
/note="Alignment: CDS, | Intron"
/evidence-not_experimental
5209. .5264
/note="Alignment: CDS, |CG415001|89.3|845|900"
/evidence-not_experimental
complement(5238..5431)
/note="BLASTN (EMBL), 1. .194 of emb|G30851|HS1140038 human
chromosome 7 STR SWS3840; single read."
/note="Region: Data base match"
/evidence-not_experimental
5757. .14176
/note="GC score = 489.57 (8420bp)"
/note="Region: GC content"
/evidence-not_experimental
5844. .7208
/note="CpG island score = 0.79, GC = 69.50%, CpGs = 126"
/note="Region: CpG island"
/evidence-not_experimental
6019. .6471
/note="CpG core score = 8.90"
/note="Region: CpG island"
/evidence-not_experimental
6454. .6508
/note="homology = 89.10%, score = 38, counts = 11"
/rpt_type-tandem
/rpt_unit-ctctcc
/evidence-not_experimental
complement(6738..7007)
/note="Alignment: CDS,
|HSACH3|98.9|69|339|OC050362|86.6|1|167|MMACHE2|96.1|1|77
|S508792|98.7|1|77"
/evidence-not_experimental
complement(6781..7047)
/note="BLASTN (EMBL), 1873. .2139 of emb|M55040|HSACHE

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alignment_scores:
Quality: 14.00
Ratio: 1.000

Length: 14
Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x HSAF002993/rev

Align seg 1/1 to reverse of: HSAF002993 from: 1 to: 34921

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
6975 GCCGAGTTCACCGCTGAGCTCTACATGGTGCCTGGAAG 6934

seq_name: gb_htg29:AC011895

seq_documentation_block:

LOCUS AC011895 175155 bp DNA HTG 21-APR-2000
DEFINITION Homo sapiens chromosome 7 clone RP11-126L15, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
ACCESSION AC011895
VERSION AC011895.3 GI:7630854
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Waterston,R.H.

TITLE The sequence of Homo sapiens clone

JOURNAL

UNPUBLISHED

REFERENCE

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL

Submitted (15-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

On Apr 21, 2000 this sequence version replaced gi:6136444.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

----- Project Information -----

Center project name: H.NH0126L15

----- Summary Statistics -----

Sequencing vector: M13; 74%

Chemistry: Dye-primer ET; 67% of reads

Chemistry: Dye-terminator Big Dye; 33% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 173580 bases at least Q40

Consensus quality: 173920 bases at least Q30

Consensus quality: 174136 bases at least Q20

Insert size: 184000; agarose-fp

Insert size: 174955; sum-of-contigs

Quality coverage: 7.01 in Q20 bases; agarose-fp

Quality coverage: 7.40 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 28804: contig of 28804 bp in length

* 28805 28904: gap of unknown length

* 28905 93340: contig of 64436 bp in length

* 93341 93440: gap of unknown length

* 93441 175155: contig of 81715 bp in length.

Location/Qualifiers

1..175155

/organism="Homo sapiens"

/db_xref="taxon:9606"

FEATURES

SOURCE

/chromosome="7"
/clone="RP11-126L15"
BASE COUNT 40525 a 45733 c 46176 g 42521 t 200 others
ORIGIN

alignment_scores:

Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AC011895/rev

Align seg 1/1 to reverse of: AC011895 from: 1 to: 175155

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14

|||||
135235 GCCGAGTTCACCGCTGAGCTCTACATGGTGCCTGGAAG 135194

seq_name: gb_ov:AF030422

seq_documentation_block:

LOCUS AF030422 4472 bp DNA VRT 20-NOV-1997
DEFINITION Electrophorus electricus acetylcholinesterase catalytic subunit
precursor gene, complete cds.

ACCESSION AF030422

VERSION AF030422.1 GI:2613035

KEYWORDS

electric eel.

SOURCE

Electrophorus electricus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;
Gymnotidae; Electrophoridae; Electrophorus.

REFERENCE

1 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Cloning and expression of acetylcholinesterase from Electrophorus

J. Biol. Chem. (1997) In press

REFERENCE

2 (bases 1 to 4472)

AUTHORS Simon,S. and Massoulié,J.

TITLE Direct Submission

Submitted (15-OCT-1997) Neurobiology, Ecole Normale Supérieure, 46

Rue d'Ulm, Paris 75005, France

FEATURES

source

1..4472

/organism="Electrophorus electricus"

/db_xref="taxon:8005"

118..186

Join(118..1525,1694..1886,2052..2230,3582..3703)

/EC_number="3.1.1.7"

/note="type T catalytic subunit"

/codon_start=1

/product="acetylcholinesterase catalytic subunit

precursor"

/protein_id="AAB86606.1"

/db_xref="GI:2613036"

/translation="MKILDALLPPIFMFFIHLSTADTPELTIMRLGQVGTPLP
VPDRSHVIAELGIPAEPLGKREPKKPNVDFADYPYACQYVDYSYGF
SGTEWNPANRMSEDCILNVPAPRPHNLVWVITGGYISGSSLDVYDGRIL
AHSEKVVVSMNRYSAFALNGSAEPGNVGLLDQRLALQVQDNTHFFGNGPKQ
VTIFESAGASVGMHLLSPDRPKFTAILQSGVNGPWRVTSFDEARRAIKGLR
VGPCDGNDDTLIDCLRSKQPDLDQEWLPSFGLFRFSFVPIGVVFPDTPAAIL
NSGNFKDTQILLVQNGESFYLYGAPGSKDNESLITREDFLOQVKMSVPHANEIG
LEAVILQYDMDEDNPDKNEAMDDIVGDHNVCPLOHAKMAQYSILOQGTCTAS
QGNLWGNSGASNSGNSQSVLYLWDFDRASNLVPEWNGVHIGYEIEVFGLPLEK
RLNTLLEEKLSRMKMYWANFARTGNINVDGSDISRRRWPFVFTSEKQHVGLNTD
SLKVKHGLKSQFCALNWRFLPRLNLVTENIDDAERQWKAEEFHWSSYMMHWNKQFDHY
SKQERCTNL"
-mRNA
Join(118..1525,1694..1886,2052..2230,3582..3703);
/product="acetylcholinesterase catalytic subunit
precursor"
Join(187..1525,1694..1886,2052..2230,3582..3700)
/note="acetylcholinesterase catalytic subunit"

mat_peptide

BASE COUNT 1234 a 904 c 983 g 1351 t
ORIGIN

alignment_scores:

Quality: 10.00 Length: 10
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AF030422 ..

Align seg 1/1 to: AF030422 from: 1 to: 4472

1 AlaGlupHeHisArgTrpSerSerTyrMet 10

|||||
3614 GCAGAGTCCACCGAGTGCATG 3643

seq_name: gb_ov:TMACHE2

seq documentation_block:

LOCUS TMACHE2 605 bp mRNA VRT 14-JUL-1995
DEFINITION Torpedo marmorata mRNA fragment for acetylcholinesterase C-term.
(pACHE2).

ACCESSION X13172

VERSION X13172.1 GI:64416

KEYWORDS acetylcholinesterase; alternative splicing.

SOURCE marbled electric ray.

ORGANISM

Torpedo marmorata

Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;

Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.

1 (bases 1 to 605)

Sikorav,J.L., Duval,N., Anselmet,A., Bon,S., Krejci,E., Legay,C.,

Osterlund,M., Reimund,B. and Massoulie,J.

Complex alternative splicing of acetylcholinesterase transcripts in

Torpedo electric organ; primary structure of the precursor of the

glycolipid-anchored dimeric form

EMBO J. 7 (10), 2983-2993 (1988)

JOURNAL 89030590

MEDLINE

COMMENT See also X13173, X13174 and X05497

FEATURES

Source

1..605

Location/Qualifiers

/organism="Torpedo marmorata"

/db_xref="taxon:7788"

/tissue_type="electric organ."

/clone="pACHE2"

/note="common mRNA sequence"

<1..103

<1..225

/codon_start=1

/product="acetylcholinesterase (74 AA)"

/protein_id="CAA31370.1"

/db_xref="GI:64417"

/db_xref="SWISS-PROT:P07692"

/translation="FIDLNTEPIKQRLVQVFCVFNQFLPKLLNATETIDEAERQW

KTEFHWSYMMHWKQFDQYSRHENCAEL"

104..>605

/note="unique mRNA sequence of pACHE2"

127 a 228 c 117 g 133 t

alignment_scores:

Quality: 9.00 Length: 9
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x TMACHE2 ..

Align seg 1/1 to: TMACHE2 from: 1 to: 605

2 GlupHeHisArgTrpSerSerTyrMet 10
|||||
139 GAGTTTCATCGGTGGAGTTCCTACATG 165

OM of: US-09-155-076-1 to: N_Geneseq_36:* out_format : pfs

Date: Sep 13, 2000 3:50 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet.p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US09155076/runat_29082000_092539_16943/app_query.fasta_1.144
-DB=N_Geneseq_36 -QFMT=fastcap -SUFFIX=ring -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAXLEN=100000 -USER=US09155076.ecgnl_1_75 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1

Query length: 14

Database: N_Geneseq_36:*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.910000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000

WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_36:Q05999	+	14.00	275.66	9.4e-08	1800	Sequence encoding foetal human
N_Geneseq_36:Q05998	+	14.00	274.13	1.1e-07	2256	Sequence encoding human acetyl
N_Geneseq_36:Q99002	+	14.00	274.14	1.1e-07	2256	Human acetylcholinesterase (AC
N_Geneseq_36:774084	-	6.00	116.61	67.94	1237	Feline immunodeficiency virus
N_Geneseq_36:747239	-	6.00	116.01	73.38	1353	FIV gag gene. Recombinant rac
N_Geneseq_36:749076	-	6.00	116.01	73.38	1353	Feline immunodeficiency virus
N_Geneseq_36:Q85985	-	6.00	115.69	76.40	1418	gag gene of NCSU1 strain of fe
N_Geneseq_36:V84600	-	6.00	114.45	89.61	1707	Human secreted protein gene 19
N_Geneseq_36:784434	-	6.00	109.06	178.86	3815	DNA encoding one known and fou
N_Geneseq_36:V53496	-	6.00	109.06	178.86	3815	DNA encoding a Staphylococcus
N_Geneseq_36:V74531	+	6.00	100.81	515.01	13059	Staphylococcus aureus contig
N_Geneseq_36:V30458_4	-	6.00	86.53	3.2e+03	110000	Continuation (5 of 6) of V3
N_Geneseq_36:V30459_4	-	6.00	86.53	3.2e+03	110000	Continuation (5 of 6) of V3
N_Geneseq_36:Q67988	+	5.00	124.05	26.15	20	Sequence of PCR primer for HBV S
N_Geneseq_36:V75042	+	5.00	122.83	30.59	24	Rat hexokinase I gene PCR primer
N_Geneseq_36:V00113	+	5.00	122.83	30.59	24	Hexokinase PCR primer SEQ ID NO:
N_Geneseq_36:V00151	+	5.00	122.83	30.59	24	Hexokinase PCR primer SEQ ID NO:
N_Geneseq_36:V75202	+	5.00	122.83	30.59	24	Primer 2 used in an assay for ta
N_Geneseq_36:V61232	+	5.00	121.12	38.11	31	Cellular apoptosis susceptibility
N_Geneseq_36:V11589	+	5.00	118.62	52.50	45	Oligonucleotide L4 for monellin
N_Geneseq_36:V11581	+	5.00	118.62	52.50	45	Oligonucleotide U3 for monellin
N_Geneseq_36:V72037	+	5.00	116.36	70.10	63	Human CP2 PCR primer CME 00399.
N_Geneseq_36:V65258	+	5.00	113.54	100.68	96	Platelet derived growth factor A
N_Geneseq_36:V84383	+	5.00	111.99	122.84	121	Friedreich's ataxia STM7 gene
N_Geneseq_36:V89719	+	5.00	111.99	122.84	121	EST clone Cn771. New polynucle
N_Geneseq_36:V89401	+	5.00	107.77	210.95	227	Methods for diagnosing Friedrei
N_Geneseq_36:V25215	+	5.00	106.94	234.70	257	Human gene signature HUMG07376
N_Geneseq_36:V26052	+	5.00	106.46	250.31	276	Human gene signature HUMG08288
N_Geneseq_36:V06032	+	5.00	106.44	250.31	277	Human brain Expressed Sequence
N_Geneseq_36:V70902	+	5.00	106.32	254.19	282	ORF 9 from MYM complementary s
N_Geneseq_36:V87692	+	5.00	106.32	254.19	282	EST clone EN271. New polynucle
N_Geneseq_36:V93187	+	5.00	106.25	256.51	285	Sequence encoding single chain
N_Geneseq_36:Q50695	+	5.00	106.25	256.51	285	Monellin single-chain analogue.
N_Geneseq_36:V09154	+	5.00	106.25	256.51	285	Single chain form monellin anal
N_Geneseq_36:V11578	+	5.00	106.25	256.51	285	Single-chain monellin synthetio
N_Geneseq_36:V93527	+	5.00	106.25	256.51	285	DNA encoding single-chain form
N_Geneseq_36:V89115	+	5.00	106.25	256.51	285	Synthetic gene encoding single
N_Geneseq_36:V17095	+	5.00	106.25	256.51	285	Single chain monellin protein a
N_Geneseq_36:Q48036	+	5.00	106.09	261.92	292	"Fused monellin" gene. New recd

N_Geneseq_36:Q21454 - 5.00 106.00 265.00 296
N_Geneseq_36:V77456 + 5.00 105.86 289.61 302
N_Geneseq_36:Q61097 + 5.00 105.25 291.71 331
N_Geneseq_36:V27413 + 5.00 105.19 293.99 334
N_Geneseq_36:V78736 + 5.00 105.07 298.52 340
N_Geneseq_36:V20283 - 5.00 104.83 307.55 352

seq_name: N_Geneseq_36:Q05999

seq_documentation_block:

ID Q05999 standard; DNA; 1800 BP.

AC Q05999;

DT 16-JAN-1991 (first entry)

DE Sequence encoding foetal human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

OS megakaryocytopoiesis; ovarian cancer; ds.

EH Homo sapiens.

FT cds

FT 1..1500

FT /*tag= a

FT 1501..1800

FT /*tag= b

FN EP-388906-A.

PD 26-SEP-1990.

PF 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS) YISSUM RES DEV CO.

PI Soreq H, Zakut H;

DR WPI; 90-291865/39.

DR P-PSDB; R06990.

PT Human acetylcholinesterase DNA and prodn. of recombinant hACHE -

PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-

PT cytoositic disorders and ovarian carcinomas.

PS Disclosure; Fig 1c; 47pp; English.

CC hACHE is useful as an active pharmacological component for the

CC prophylaxis and treatment of organophosphorous poisoning, and

CC post-surgical apnea due to succinylcholine administration.

CC cDNA probe to the sequence may be used in diagnosis of various

CC leukaemias, abnormal megakaryocytopoiesis and ovarian carcinomas.

CC Bases given as N are obscured in the patent specification.

SQ Sequence 1800 BP; 330 A; 602 C; 539 G; 326 T;

alignment_scores:

Quality: 14.00

Ratio: 1.000

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x Q05999

Align seg 1/1 to: Q05999 from: 1 to: 1800

1 AlaGluPHisHArgTrpSerTyrMetValHisTrpLys 14
|||||
1414 GCCGAGTTCACGCGTGGAGTCTCATACATGTCACATGGGAG 1455

seq_name: N_Geneseq_36:Q05998

seq_documentation_block:

ID Q05998 standard; DNA; 2253 BP.

AC Q05998;

DT 16-JAN-1991 (first entry)

DE Sequence encoding human acetylcholinesterase (hACHE).

KW Organophosphorous poisoning; OP; cancer; leukaemia;

OS megakaryocytopoiesis; ovarian cancer; ds.

EH Homo sapiens.

FT EP-388906-A.

PD 26-SEP-1990.

PF 20-MAR-1990; 105274.

PR 21-MAR-1989; IL-089703.

PA (YISS) YISSUM RES DEV CO.

PI Soreq H, Zakut H;

DR WPI; 90-291865/39.

DR P-PSDB; R06989.
PT Human acetylcholinesterase DNA and prodn. of recombinant hAChE -
PT for treatment of organo-phosphorous poisoning and diagnosis of haemo-
PT cytopoietic disorders and ovarian carcinomas.

PS Claim 5; Page 25; 47pp; English.
CC Gene product is useful as an active pharmacological component for the
CC treatment of organo-phosphorous poisoning, and post-
CC prophylaxis and treatment of organophosphorus administration.
CC surgical apnea due to succinylcholine administration.
CC cDNA probe to the sequence may be used in diagnosis of various
CC leukemias, abnormal megakaryocytopoiesis and ovarian carcinomas.
SQ Sequence 2253 BP; 390 A; 740 C; 594 G; 429 T;

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x Q05998

Align seg 1/1 to: Q05998 from: 1 to: 2253

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
1912 GCCGAGTTCACCGCTGAGCTCTACATGGTGCCTGGAAG 1953

seq_name: N_Geneseq_36:Q99002

seq_documentation_block:

ID Q99002 standard; DNA; 2256 BP.

AC Q99002;
DE 31-MAR-1996 (first entry)
DE Human acetylcholinesterase (ACHE) gene.
KW Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7;
KW chromosome-7q22; acetylcholine-hydrolyzing enzyme; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 160..2206

FT /*tag= a

PN W09523158-AL.

PD 31-AUG-1995.

PF 28-FEB-1995; U02806.

PR 28-FEB-1994; US-202755.

PR 09-JAN-1995; US-370156.

PA (KOHN/) KOHN K I.

PA (YISS) YISSUM RES & DEV CO.

PI Shani M, Soreq H, Zakut H;

DR WPI; 95-311499/40.

DR P-PSDB; R80726.

PT Alternative forms of human acetyl cholinesterase (ChE) gene -
PT expressed in transgenic animal assay system for evaluating anti-ChE
PT activity of organo:phosphate(s), etc. or as model of ChE imbalance

PS Claim 3; Fig.1A; 55pp; English.

CC This DNA sequence encoding human acetylcholinesterase is useful

CC for producing transgenic animals which express AChE. The

CC transgenic animals are in turn useful as an assay system for

CC determining the anti-ChE activity of organophosphates, carbamates,

CC anti-ChE drugs, plant glycoalkaloids and snake venoms. This gene

CC contains a promoter region, 6 exons (E1 to E6) and 4 introns (I1-

CC I4).

SQ Sequence 2256 BP; 390 A; 757 C; 680 G; 429 T;

alignment_scores:

Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x Q99002

Align seg 1/1 to: Q99002 from: 1 to: 2256

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
1915 GCCGAGTTCACCGCTGAGCTCTACATGGTGCCTGGAAG 1956

seq_name: N_Geneseq_36:T74084

seq_documentation_block:

ID T74084 standard; DNA; 1237 BP.

AC T74084;

DE 24-SEP-1997 (first entry)

DE Feline immunodeficiency virus p10 encoding DNA with deletion.

DE FIV p10; nucleocapsid; virion; vaccine; cat; ss.

KW Feline immunodeficiency virus

OS Feline immunodeficiency virus

FH Key Location/Qualifiers

FT cds 1..1237

FT /*tag= a

FT /product= FIV_p10

FT /note= "With a deleted section that encodes the

FT nucleocapsid (p10) protein"

FN W09640953-AL.

PD 19-DEC-1996.

PF 03-JUN-1996; U08639.

PR 07-JUN-1995; US-479703.

PA (AMHP) AMERICAN HOME PROD CORP.

PI Chavez LG, Huang C, Wasmoen T;

DR WPI; 97-065191/06.

DR P-PSDB; W23543.

PT Plasmid encoding feline immunodeficiency virus with incomplete

PT nucleocapsid p10 protein - for production of virion(s) lacking

PT packaged RNA useful in FIV vaccines

PS Claim 1; Page -; 36pp; English.

CC The present sequence encodes the feline immunodeficiency virus

CC (FIV) p10 genome, in which nucleotides encoding at least part of the

CC nucleocapsid (p10) protein have been deleted from the gag gene.

CC FIV virions which lack nucleocapsid protein p10 are used in vaccines

CC to prevent or reduce disease caused by FIV in cats. Protein p10 is

CC responsible for packaging RNA into virions, deletion of part of the

CC nucleocapsid protein will result in empty, and therefore, non-

CC infectious FIV virions.

CC N.B. The present sequence does not appear in the specification but

CC has been derived from the sequence in figure 2.

SQ Sequence 1237 BP; 433 A; 216 C; 298 G; 290 T;

alignment_scores:

Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x T74084/rev

Align seg 1/1 to reverse of: T74084 from: 1 to: 1237

3 PheHisArgTrpSerSer 8

|||||

366 TTTCATAGTGGTCTAGT 349

seq_name: N_Geneseq_36:T747239

seq_documentation_block:

ID T47239 standard; DNA; 1353 BP.

AC T47239;

DT 06-APR-1997 (first entry)

DE FIV gag gene.

KW FIV; gag gene; env gene; racoon poxvirus; recombinant vaccine; ds.

OS Feline immunodeficiency virus strain NCSU-1.

FH Key Location/Qualifiers

FT primer_bind complement (857..880)

FT /*tag= a

FT /note= "5' primer binding region"

```

FT primer_bind 1513..1535
FT /*tag= b
FT /*note= '3' primer binding region"
PN W09640258-A1.
PD 19-DEC-1996.
PF 03-JUN-1996; U08508.
PR 07-JUN-1995; US-482090.
PA (AMHP ) AMERICAN HOME PROD CORP.
PI Chavez LG, Chu H, Wasmoen T;
DR WPI; 97-051908/05.
DR P-PSDB; W07847.
PT Recombinant raccoon poxvirus - with at least 1 internal gene
PT encoding feline immunodeficiency virus env or gag protein, useful in
PT vaccine for prophylaxis of disease
PS Claim 11; Fig 5A-C; 50pp; English.
CC The FIV gag gene (T47238), encoding the FIV gag protein (W07847) can
CC be included in recombinant raccoon poxviruses (RRPV) to provide
CC recombinant vaccines that protect felines from FIV infection. The
CC gag gene was obtd. by PCR amplification (see also T47246-47) and
CC cloned into pS11190. Vero cells were infected with wild-type RRV
CC (ATCC VR-838) and then transfected with pS111-FIV gag to obtain
CC the RRPV. Other RRPVs may include DNA sequences encoding FIV
CC env (see also T47238), envAB or immunogenic fragments of FIV env
CC and gag.
SQ Sequence 1353 BP; 480 A; 230 C; 325 G; 318 T;

```

```

alignment_scores:
  Quality: 6.00 Length: 6
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-1 x T47238/rev ..
Align seg 1/1 to reverse of: T47239 from: 1 to: 1353

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```

3 PheHisArgTrpSerSer 8
|||||
366 TTTCATAGATGGCTAGT 349

```

```

seq_name: N_Geneseq_36:T49076

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```

seq_documentation_block:
ID T49076 standard; DNA; 1353 BP.
AC T49076;
DT 24-SEP-1997 (first entry)
DE Feline immunodeficiency virus gag gene encoding DNA.
KW FIV p10; nucleocapsid; virion; vaccine; cat; ss.
OS Feline immunodeficiency virus.
FH key Location/Qualifiers
FT cds 1..1353
FT /*tag= a
FT misc_feature 1126..1241
FT /*tag= b
FT /*note= "Can delete this segment of nucleotides
FT encoding the nucleocapsid (p10) protein"
PN W09640953-A1.
PD 19-DEC-1996.
PF 03-JUN-1996; U08639.
PR 07-JUN-1995; US-479703.
PA (AMHP ) AMERICAN HOME PROD CORP.
PI Chavez LG, Huang C, Wasmoen T;
DR WPI; 97-065191/06.
DR P-PSDB; W08435.
PT Plasmid encoding feline immunodeficiency virus with incomplete
PT nucleocapsid p10 protein - for production of virion(s) lacking
PT packaged RNA useful in FIV vaccines
PS Claim 2; Fig 2; 36pp; English.
CC The present sequence encodes the feline immunodeficiency virus
CC (FIV) gag gene, which contains the nucleotides encoding the whole
CC nucleocapsid (p10) protein. In a preferred example of the FIV

```

```

CC nucleotide sequence the nucleotides encoding the nucleocapsid (p10)
CC protein (or a portion of them) are deleted from the gag gene, see
CC features table. FIV virions which lack nucleocapsid protein p10 are
CC used in vaccines to prevent or reduce disease caused by FIV in cats.
CC Protein p10 is responsible for packaging RNA into virions, deletion
CC of part of the nucleocapsid protein will result in empty, and
CC therefore, non-infectious FIV virions.
SQ Sequence 1353 BP; 479 A; 229 C; 327 G; 318 T;

```

```

alignment_scores:
  Quality: 6.00 Length: 6
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:
US-09-155-076-1 x T49076/rev ..

```

```

Align seg 1/1 to reverse of: T49076 from: 1 to: 1353

```

```

3 PheHisArgTrpSerSer 8
|||||
366 TTTCATAGATGGCTAGT 349

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seq_name: N_Geneseq_36:Q85885

```

```

seq_documentation_block:
ID Q85885 standard; cDNA; 1418 BP.
AC Q85885;
DT 24-OCT-1995 (first entry)
DE gag gene of NCSU1 strain of feline immunodeficiency virus.
KW Feline immunodeficiency virus; FIV; CD8; antigen; vaccine;
KW diagnosis; primer; probe; acquired immune deficiency syndrome; AIDS;
KW model system; screening; long terminal repeat; LTR; ss.
OS Feline immunodeficiency virus (NCSU1 strain).
FH key Location/Qualifiers
FT cds 23..1375
FT /*tag= a
FT /*product= NCSU1 FIV gag gene product.
PN W09505450-A.
PD 23-FEB-1995.
PF 25-JUL-1994; U08364.
PR 03-SEP-1991; US-752424.
PR 12-AUG-1993; US-105710.
PA (UYNQ-) UNIV NORTH CAROLINA STATE.
PI Tompkins MB, Tompkins WAF;
DR WPI; 95-098760/13.
DR P-PSDB; R71479.
PT New isolate of feline immunodeficiency virus - and infected host
PT cells, DNA, vectors and infected cats, useful in vaccines and as
PT models for human AIDS
PS Example 12; Page 38-40; 50pp; English.
CC The NCSU1 strain (ATCC VR2333) of the feline immunodeficiency virus
CC (FIV) is highly infectious in vivo and causes a rapid inversion of
CC the CD4+CD8+ ratio in infected animals. Antigenic fragments of the
CC virus can be used in vaccines. Fragments of the DNA can also be used
CC diagnostically as probes and primers and for expressing viral
CC antigens. Cats infected with the virus are useful as model systems
CC for studying AIDS and for screening therapeutic drugs. Two primers
CC (Q85883, Q85884) were used to amplify the gag gene of the NCSU1
CC strain of FIV for its subcloning and subsequent sequencing.
SQ Sequence 1418 BP; 506 A; 239 C; 341 G; 332 T;

```

```

alignment_scores:
  Quality: 6.00 Length: 6
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

```

alignment_block:
US-09-155-076-1 x Q85885/rev ..

```

```

Align seg 1/1 to reverse of: Q85885 from: 1 to: 1418

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Wed Sep 13 08:11:26 2000

us-09-155-076-1-1.rng

3 PheHisArgTyrSerSer 8
 |||||

388 TTTCATAGATGGTCTAGT 371

seq_name: N_Geneseq_36.V84600

seq_documentation_block:

ID_V84600 standard; DNA; 1707 BP.

AC V84600; 1999 (first entry)
 DT 01-MAR-1999 (first entry)
 DE Human secreted protein gene 190 clone HIASB53.
 KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 OS Homo sapiens.
 PN W09854963-A2.
 PD 10-DEC-1998
 PF 04-JUN-1998; U11422
 PR 18-DEC-1997; US-070923.
 PR 06-JUN-1997; US-048877.
 PR 06-JUN-1997; US-048881.
 PR 06-JUN-1997; US-048884.
 PR 06-JUN-1997; US-048893.
 PR 06-JUN-1997; US-048896.
 PR 06-JUN-1997; US-048899.
 PR 06-JUN-1997; US-048915.
 PR 06-JUN-1997; US-048949.
 PR 06-JUN-1997; US-048964.
 PR 06-JUN-1997; US-048972.
 PR 06-JUN-1997; US-049020.
 PR 06-JUN-1997; US-049375.
 PR 05-SEP-1997; US-057628.
 PR 05-SEP-1997; US-057635.
 PR 05-SEP-1997; US-057644.
 PR 05-SEP-1997; US-057647.
 PR 05-SEP-1997; US-057650.
 PR 05-SEP-1997; US-057661.
 PR 05-SEP-1997; US-057667.
 PR 05-SEP-1997; US-057761.
 PR 05-SEP-1997; US-057764.
 PR 05-SEP-1997; US-057770.
 PR 05-SEP-1997; US-057775.
 PR 05-SEP-1997; US-057778.
 PR 06-JUN-1997; US-048875.
 PR 06-JUN-1997; US-048878.
 PR 06-JUN-1997; US-048882.
 PR 06-JUN-1997; US-048885.
 PR 06-JUN-1997; US-048894.
 PR 06-JUN-1997; US-048897.
 PR 06-JUN-1997; US-048900.
 PR 06-JUN-1997; US-048916.
 PR 06-JUN-1997; US-048962.
 PR 06-JUN-1997; US-048970.
 PR 06-JUN-1997; US-048974.
 PR 06-JUN-1997; US-049373.
 PR 05-SEP-1997; US-057584.
 PR 05-SEP-1997; US-057629.
 PR 05-SEP-1997; US-057642.
 PR 05-SEP-1997; US-057645.
 PR 05-SEP-1997; US-057648.
 PR 05-SEP-1997; US-057651.
 PR 05-SEP-1997; US-057662.
 PR 05-SEP-1997; US-057668.
 PR 05-SEP-1997; US-057669.
 PR 05-SEP-1997; US-057672.
 PR 05-SEP-1997; US-057675.
 PR 05-SEP-1997; US-057771.
 PR 05-SEP-1997; US-057776.

PR 06-JUN-1997; US-048876.
 PR 06-JUN-1997; US-048880.
 PR 06-JUN-1997; US-048883.
 PR 06-JUN-1997; US-048892.
 PR 06-JUN-1997; US-048895.
 PR 06-JUN-1997; US-048898.
 PR 06-JUN-1997; US-048901.
 PR 06-JUN-1997; US-048917.
 PR 06-JUN-1997; US-048963.
 PR 06-JUN-1997; US-048971.
 PR 06-JUN-1997; US-049019.
 PR 06-JUN-1997; US-049374.
 PR 05-SEP-1997; US-057627.
 PR 05-SEP-1997; US-057634.
 PR 05-SEP-1997; US-057643.
 PR 05-SEP-1997; US-057646.
 PR 05-SEP-1997; US-057649.
 PR 05-SEP-1997; US-057654.
 PR 05-SEP-1997; US-057666.
 PR 05-SEP-1997; US-057760.
 PR 05-SEP-1997; US-057763.
 PR 05-SEP-1997; US-057769.
 PR 05-SEP-1997; US-057774.
 PR 05-SEP-1997; US-057777.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA,
 PI Fan P, Feng P, Ferrie AM, Fischer CL, Florence C,
 PI Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW,
 PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM,
 PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
 DR WPI: 99-059865/05.
 DR P-PSDB; W88723, W89065, W89066, W89067, W89068, W89069, W89070, W89071,
 DR W89072.
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS Claim 4: Page 452-453; 772pp; English.
 CC The invention relates to nucleic acid sequences (V84411 to V84633)
 CC encoding human secreted proteins (W88534 to W88756). The secreted protein
 CC gene sequences are deposited with the ATCC under deposit numbers ATCC
 CC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
 CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
 CC cells comprising recombinant vectors containing the nucleic acid
 CC sequences are used for the recombinant production of the secreted
 CC proteins. The polynucleotide and amino acid sequences are useful for are
 CC useful for preventing, treating or ameliorating medical conditions e.g.
 CC by protein or gene therapy. Pathological conditions can be also diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the polynucleotides, based on
 CC which tissues they are most highly expressed in, and include developing
 CC products for the diagnosis or treatment of cancer, neurodegenerative
 CC disorders, developmental abnormalities and foetal deficiencies, blood
 CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
 CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
 CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
 CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
 CC such as osteoporosis, arthritis or malignancies, diseases of testes, lung
 CC or thymus, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The present sequence represents a gene encoding a human secreted protein
 CC (see descriptor line for gene number and clone identification).
 CC Sequence 1707 BP; 469 A; 316 C; 368 G; 552 T;
 SQ

alignment_scores:

Quality: 6.00

Length: 6

Ratio: 1.000

Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x W84600/rev ..

Align seg 1/1 to reverse of: V84600 from: 1 to: 1707

6 TrpSerTyrMetVal 11
|||||
750 TGGTCTCTATATGGTT 733

seq_name: N_Geneseq_36.T84154

seq_documentation_block:

ID T84154 standard; DNA; 3815 BP.
AC T84154;
DT 07-SEP-1998 (first entry)
DE DNA encoding one known and four unknown Staphylococcus aureus proteins.
KW Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW Staphylococcal gene; regulatory element; bacterial gene expression;
KW vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
KW toxic shock syndrome; ss.
OS Staphylococcus aureus.
FH Key Location/Qualifiers
CDS 257..934
FT /*tag= a
FT /product= "Preprotein translocase SECY subunit"
FT 945..1280
FT /*tag= b
FT /product= "Encodes protein W28243"
FT 1610..2362
FT /tag= c
FT /product= "Encodes protein W28244"
FT 3173..3364
FT /*tag= d
FT /product= "Encodes protein W28245"
FT 3380..3559
FT /*tag= e
FT /product= "Encodes protein W28246"
FT W09730070-A1.
PN 21-AUG-1997.
PD 19-FEB-1997; U02318.
PF 19-FEB-1996; US-011888.
PR 20-FEB-1996; US-011888.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Black M, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
PI Pratt JM, Reichard RW, Rosenberg M, Ward JM;
PI WPI: 97-424969/39.
DR P-PSDB; W28243, W28244, W28245, W28246.
DT Novel polypeptide(s) from Staphylococcus aureus strain WCNU29 - used
PT to isolate antimicrobial compounds, and in vaccines against S.
PT aureus infection
PS Claim 9; Pages 915-916; 989pp; English.
CC The present sequence encodes four Staphylococcus aureus proteins of
CC unknown function. The sequence also encodes a Staphylococcus aureus
CC protein, that, based on homology with a Bacillus subtilis protein,
CC is believed to be a preprotein translocase SECY subunit. The present
CC sequence was obtained from a library of clones of S. aureus WCNU 29
CC in Escherichia coli. The DNA sequence can be used in the construction
CC of ribosomes and antisense sequences to control the expression of
CC Staphylococcal genes. The DNA sequence is also useful as a source of
CC regulatory elements for the control of bacterial gene expression. The
CC encoded protein may be used to produce vaccines to enable a host to
CC produce specific antibodies with antibacterial action. These vaccines
CC and antibodies would protect a host against invasion by S. aureus, and
CC conditions relating to Staphylococcal infection, e.g. Staphylococcal
CC food poisoning, scaled skin syndrome, and toxic shock syndrome.
CC Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;
SQ

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x T84154/rev ...

Align seg 1/1 to reverse of: T84154 from: 1 to: 3815

4 HisArgTrpSerTyr 9
|||||
985 CATCGTTGGTCATCGTAC 968

seq_name: N_Geneseq_36.V53496

seq_documentation_block:

ID V53496 standard; DNA; 3815 BP.
AC V53496;
DT 30-OCT-1998 (first entry)
DE DNA encoding a Staphylococcus aureus protein of unknown function.
KW Staphylococcus aureus protein; immune response induction; eye infection;
KW antibody production; T-cell immune response; gastrointestinal infection;
KW respiratory infection; inhibitor; bacterial infection; cardiac infection;
KW central nervous system; kidney infection; urinary tract infection;
KW antimicrobial compound identification; broad spectrum antibiotic;
KW therapy; ss.
OS Staphylococcus aureus.
PN EP-841394-A2.
PD 13-MAY-1998.
PF 24-SEP-1997; 307485.
PR 24-SEP-1996; US-027032.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Black M, Burnham MKR, Hodgson JE, Knowles DJC,
PI Lonetto MA, Nicholas RO, Pratt JM, Reichard RW, Rosenberg M,
PI Ward JM;
PI WPI: 98-252940/23.
DR P-PSDB; W77704.
DT New nucleic acid sequences from Staphylococcus aureus WCNU29 -
PT useful in vaccines and for treatment of bacterial infections of e.g.
PT respiratory tract and central nervous system
PS Claim 1; Page 160-162; 390pp; English.
CC This sequence encodes a Staphylococcus aureus protein of unknown
CC function, and represents a DNA sequence of the invention.
CC The DNA sequences were isolated from Staphylococcus aureus WCNU29
CC (NCIMB 40771). Host cells containing the DNA sequences are used to
CC produce polypeptides or fragments. The proteins are used in the treatment
CC of disease, for inducing an immune response by administering them, to
CC produce antibody and/or T-cell immune response. Antagonists of the
CC proteins are used for the inhibition of bacterial polypeptides.
CC Conditions which may be treated include bacterial infections, especially
CC respiratory, cardiac, gastrointestinal, central nervous, eye, kidney,
CC urinary tract, skin, bones and joints. The proteins can also be used to
CC identify antimicrobial compounds which are broad spectrum antibiotics,
CC especially useful in the treatment of H. pylori infection.
SQ Sequence 3815 BP; 1267 A; 562 C; 750 G; 1199 T;

alignment_scores:
Quality: 6.00 Length: 6
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x V53496/rev ..

Align seg 1/1 to reverse of: V53496 from: 1 to: 3815

4 HisArgTrpSerTyr 9
|||||
985 CATCGTTGGTCATCGTAC 968

seq_name: N_Geneseq_36.V74531

seq_documentation_block:

ID V74531 standard; DNA; 13059 BP.
AC V74531;
DT 16-MAR-1999 (first entry)
DE Staphylococcus aureus contig SEQ ID #220.
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;

KW skin infection; surgical wound infection; scalded skin syndrome;
 OS toxic shock syndrome; ds.

FT Staphylococcus aureus;
 FH Key Location/Qualifiers
 FT misc_feature 301..360

FT /*tag= a
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 2101..2160

FT /*tag= b
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 3901..3960

FT /*tag= c
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 5701..5760

FT /*tag= d
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 7501..7560

FT /*tag= e
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 9301..9360

FT /*tag= f
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 11101..11160

FT /*tag= g
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"
 FT misc_feature 12901..12960

FT /*tag= h
 FT /note= "these bases represent a line of missing text in
 FT the sequence listing in the specification. They
 FT are included to maintain the nucleotide numbering
 FT given in the specification for this DNA sequence"

PN EP-786519-A2.

PD 30-JUL-1997.

PE 07-JAN-1997; 100117.

PR 05-JAN-1996; US-009861.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,

PI Rosen CA;

DR WPI; 97-374922/35.

PT Polynucleotide(s) and proteins derived from *Staphylococcus aureus* -
 PT stored on computer readable medium and used in the production of

PT anti-S aureus vaccines

PS Claim 1; Page 972-980; 3271pp; English.

CC This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against *S. aureus* infection. The

CC polypeptides can also be used in a kit for the immunodetection of
 CC *S. aureus* in a sample. *S. aureus* is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used
 CC for recombinant production of the polypeptides. The new DNA sequences
 CC (and their fragments) are useful as primers or probes for isolating
 CC homologues of any of the *S. aureus* DNA sequences contained on the
 CC computer readable medium.
 SQ Sequence 13059 BP; 3881 A; 2438 C; 1860 G; 4390 T;

alignment_scores:
 Quality: 6.00 Length: 6
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x V74531 ..

Align seg 1/1 to: V74531 from: 1 to: 13059

4 HisArgTrpSerTyr 9

|||||||

10149 CATGTTGGTCATCGTAC 10166

seq_name: N_Geneseq_36:V30458_4

seq_documentation_block:

Continuation (5 of 6) of V30458 from base 400001 (Rhizobium species plasmid PNGR334a.
 WP sequence split into 6 fragments LOCUS V30458 Accession V30458

WP	Fragment Name	Begin	End
WP	V30458_0	1	110000
WP	V30458_1	100001	210000
WP	V30458_2	200001	310000
WP	V30458_3	300001	410000
WP	V30458_4	400001	510000
WP	V30458_5	500001	534720

alignment_scores:
 Quality: 6.00 Length: 6
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x V30458_4/rev ..

Align seg 1/1 to reverse of: V30458_4 from: 1 to: 110000

3 PheHisArgTrpSer 8

|||||||

73348 TTTCACAGGIGGCCICT 73331

seq_name: N_Geneseq_36:V30459_4

seq_documentation_block:

Continuation (5 of 6) of V30459 from base 400001 (Rhizobium species symbiotic plasmid
 WP sequence split into 6 fragments LOCUS V30459 Accession V30459

WP	Fragment Name	Begin	End
WP	V30459_0	1	110000
WP	V30459_1	100001	210000
WP	V30459_2	200001	310000
WP	V30459_3	300001	410000
WP	V30459_4	400001	510000
WP	V30459_5	500001	536165

alignment_scores:
 Quality: 6.00 Length: 6
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x V30459_4/rev ..

Align seg 1/1 to reverse of: V30459_4 from: 1 to: 110000

3 PheHisArgTIPSerSer 8

|||||

73348 TTTCACAGGTGGTCTCT 73331

seq_name: N_Geneseq_36:Q67988

seq_documentation_block:

ID Q67988 standard; DNA; 20 BP.

AC Q67988;

DT 02-JAN-1995 (first entry)

DE Sequence of PCR primer for HBV S-region.

KW Core antigen; recombinant replicable vaccinia virus; hepatitis;

KW prevention; therapy; epitope; hepatitis B virus; PCR primer; ss.

OS Synthetic.

PN W09412617-A.

PD 09-JUN-1994.

PF 24-NOV-1993; U11474.

PR 25-NOV-1992; US-982211.

PA (TBI-) INT BIO TECHNOLOGY LAB INC.

PI Bernstein EG, Lewis T, Okeefe RW, Souw PTS;

DR WPI; 94-200247/24.

PT Prevention and treatment of hepatitis - using recombinant

PT replicable vaccinia viruses contg. hepatitis B virus surface and

PT core antigen nucleotide sequences

PS Example; Page 76; 252pp; English.

CC A construct was made consisting from the amino terminus of

CC AA residues 1-144 of core, a 1 AA spacer (D), AAS 107-163

CC of the S antigen, and a 7 AA tail (NSGLVVK). This fusion

CC polypeptide is referred to a core-S* because only a small

CC portion of the S antigen is present. A 197 bp piece of the S

CC region containing the immunogenic regions was generated by PCR

CC of pLEH-04 using primer Q67987 which hybridises from bases

CC +304 to +323 of the S region and is designed to introduce

CC a BspEI site. A second primer was Q67988 which hybridises to the

CC opposite strand from bps +500 to +481 of the S region and is designed to

CC create an EcoRI site upon amplification. The sequences of the

CC core-S* fusion in the resulting plasmid, pHTL-28, are given in

CC Q67971 and R55288.

SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T;

alignment_scores:

Quality:	5.00	Length:	5
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-155-076-1 x Q67988 ..

Align seg 1/1 to: Q67988 from: 1 to: 20

1 AlaGluPheHisArg 5

|||||

5 GCCGAATTCATAGG 19

seq_name: N_Geneseq_36:T75042

seq_documentation_block:

ID T75042 standard; DNA; 24 BP.

AC T75042;

DT 02-FEB-1998 (first entry)

DE Rat hexokinase I gene PCR primer.

KW Recombinant protein; expression; secretory cell line; RIN;

KW insulinoma; hexokinase I; insulin; diabetes; gene therapy; primer;

KW PCR; polymerase chain reaction; rat; ss.

OS Synthetic.

OS Rattus sp.

PN W09726321-A2.

PD 24-JUL-1997. U00761.

PF 17-JAN-1997; US-028427.

PR 15-OCR-1986; US-589028.

PR 19-JAN-1996; US-589028.

PA (BETA-) BETAGENE INC.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Clark SA, Halban PA, Kruse F, McGarry D, Newgard CB;

PI Northington KD, Quaade C, Thigpen AE;

DR WPI; 97-385326/35.

PT Recombinant cell engineered to provide amylin to a mammal - useful

PT to treat e.g. angiogenesis, anorexia, obesity, hypertension,

PT osteoporosis etc.

PS Example 1; Page 132; 336pp; English.

CC This primer is located in the rat hexokinase I (HKI) gene

CC downstream of a putative recombination site. It was used with a

CC primer (see T75041) located upstream of the recombination site

CC in a control PCR to detect homologous and random integrants of a

CC HKI gene replacement vector following electroporation of rat RIN

CC insulinoma cells. Interference with HKI function reduces the

CC growth rate of cells and may allow the development of engineered

CC cells that exhibit glucose-regulatable insulin secretion. The

CC invention provides methods for production of heterologous

CC polypeptides, e.g. amylin, using recombinantly engineered cell

CC lines. Also described are methods of engineering cells for high

CC level expression, methods of large-scale heterologous protein

CC production, methods for treatment of disease in vivo using viral

CC delivery systems and recombinant cell lines, and methods for

CC isolating novel amylin receptors.

SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T;

alignment_scores:

Quality:	5.00	Length:	5
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-09-155-076-1 x T75042 ..

Align seg 1/1 to: T75042 from: 1 to: 24

7 SerSerTyrMetVal 11

|||||

5 AGCTCTTACATGGT 19

OM of: US-09-155-076-1 to: Issued_Patents_NA:* out_format : pfs
Date: Sep 13, 2000 3:48 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=framat_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US09155076/runat_29082000_092539_16923/app_query.fasta_1.144
-DB-Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-DELOP=6.000 -DEPEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -WINLEN=0
-MAXLEN=100000 -USER=US09155076@cgn1_1_41 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-155-076-1
Query length: 14
Database: Issued_Patents_NA*
Database sequences: 243080
Database length: 68777915
Search time (sec): 60.430000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-26	1	14.00	279.76	4.3e-08	1215
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-732-962A-1	1	14.00	276.97	6.2e-08	1845
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-732-962A-1	1	14.00	276.97	6.2e-08	1845
/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-5	1	14.00	275.63	7.3e-08	2256
/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-1	1	14.00	275.63	7.3e-08	2256
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-7	1	14.00	257.30	7.7e-07	35060
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-482-090-13	1	6.00	115.99	57.13	1353
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-09-007-383-13	1	6.00	115.68	59.48	1418
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-105-710-6	1	6.00	115.68	59.48	1418
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-776-251-24	1	5.00	123.43	22.01	21
/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-776-251-25	1	5.00	123.43	22.01	21
/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-588-983-41	1	5.00	122.54	24.68	24
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-588-976-41	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-295-814E-14	1	5.00	122.26	25.56	25
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-09-176-607-6	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-482-090-13	1	6.00	115.99	57.13	1353
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-105-710-6	1	6.00	115.68	59.48	1418
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-105-710-6	1	6.00	115.68	59.48	1418
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/cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-588-983-41	1	5.00	122.54	24.68	24
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-588-976-41	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-295-814E-14	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-295-814E-30	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5D_COMB.seq:US-09-176-607-6	1	5.00	122.26	25.56	25
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-482-090-13	1	6.00	115.99	57.13	1353
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-105-710-6	1	6.00	115.68	59.48	1418
/c					

```
;
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/370,156
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..78
;
US-08-370-156-26

alignment_scores:
    Quality: 14.00      Length: 14
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-370-156-26 ..

Align seg 1/1 to: US-08-370-156-26 from: 1 to: 1215

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||
874 GCCGAGTTCACCGTGGAGCTCTACATGTTGCACTGGAAG 915

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-732-962A-1

seq_documentation_block:
; Sequence 1, Application US/07732962A
; Patent No. 5248604
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: EXPRESSION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: RECOMBINANT HUMAN ACETYLCHOLINESTERASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
```

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;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,962A
; FILING DATE: 19910722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
;
US-07-732-962A-1

alignment_scores:
    Quality: 14.00      Length: 14
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-07-732-962A-1 ..

Align seg 1/1 to: US-07-732-962A-1 from: 1 to: 1845

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
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1756 GCCGAGTTCACCGTGGAGCTCTACATGTTGCACTGGAAG 1797

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US92-06106-1

seq_documentation_block:
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
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Align seg 1/1 to: US-08-370-156-1 from: 1 to: 2256
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
|||||
1915 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACGGAAG 1956
seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-1

seq_documentation_block:
; Sequence 1, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 5891725thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "ACHE gene comprising exons
; DESCRIPTION: 2, 3, 4 and 6"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-814-095-1

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-814-095-1 ..
Align seg 1/1 to: US-08-814-095-1 from: 1 to: 2256
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
|||||
1915 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACGGAAG 1956
seq_name: /cgn2_6/ptodata/2/ina/5C_COMB.seq:US-08-318-826A-7
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seq_documentation_block:
; Sequence 7, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,826A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: 2391.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
; OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,
; OTHER INFORMATION: 3, 4, 5 and 6"
; US-08-318-826A-7

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-318-826A-7 ..
Align seg 1/1 to: US-08-318-826A-7 from: 1 to: 3016
1 AlaGluPheHisArgTrpSerSertyrMetValHisTrpLys 14
|||||
2675 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACGGAAG 2716
seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-5

seq_documentation_block:
; Sequence 5, Application US/08370156
; Patent No. 5932780
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;; GENERAL INFORMATION:
;; APPLICANT: Soreq, Hermona
;; APPLICANT: Zakut, Haim
;; APPLICANT: Shani, Moshe
;; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Reising, Ethington, Barnard & Perry
;; STREET: P.O. Box 4390
;; CITY: Troy
;; STATE: Michigan
;; COUNTRY: US
;; ZIP: 48099
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/370,156
;; FILING DATE:
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kohn, Kenneth I.
;; REGISTRATION NUMBER: 30,955
;; REFERENCE/DOCKET NUMBER: P-307 (Mulford)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (810) 689-3500
;; TELEFAX: (810) 689-4071
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3016 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 160..2010
US-08-370-156-5

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-370-156-5  ..

Align seg 1/1 to: US-08-370-156-5 from: 1 to: 3016

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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2675 GCCGAGTTCACCGCTGAGCTCTACATGTCGACTGGAAG 2716

seq_name: /cgn2_6/ptodata/2/ina/6_COMBO.seq:US-08-814-095-5

seq_documentation_block:
; Sequence 5, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
```

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;; COUNTRY: U.S.
;; ZIP: 48334
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/814,095
;; FILING DATE:
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Montgomery, Ilene N.
;; REGISTRATION NUMBER: 38,972
;; REFERENCE/DOCKET NUMBER: 2391.00066
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (248) 539-5050
;; TELEFAX: (248) 539-5055
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3016 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Alternatively spliced Ache
;; DESCRIPTION: comprising exons 2, 3, 4, 5 and 6"
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 160..2010
US-08-814-095-5

alignment_scores:
  Quality: 14.00      Length: 14
  Ratio: 1.000       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-1 x US-08-814-095-5  ..

Align seg 1/1 to: US-08-814-095-5 from: 1 to: 3016

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
2675 GCCGAGTTCACCGCTGAGCTCTACATGTCGACTGGAAG 2716

seq_name: /cgn2_6/ptodata/2/ina/5C_COMBO.seq:US-08-318-826A-6

seq_documentation_block:
; Sequence 6, Application US/08318826A
; Patent No. 5891725
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Eckstein, Fritz
; TITLE OF INVENTION: Synthetic Antisense
; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions
; TITLE OF INVENTION: Containing Them
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 5891725thwestern Hwy., Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,826A

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.

REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 2391.00001

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 3096 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 160..1959

OTHER INFORMATION: /note= "Splice variant: Exons 1, 2,

US-08-318-826A-6

OTHER INFORMATION: 3, 4, 5 and the translated portion of Intron 4 (readthrough)"

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x US-08-318-826A-6 ..

Align seg 1/1 to: US-08-318-826A-6 from: 1 to: 3096

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14
|||||
2755 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 2796

seq_name: /cgn2_6/ptodata/2/ina/5D_COMB.seq:US-08-370-156-3

seq_documentation_block:

Sequence 3, Application US/08370156

Patent No. 5932780

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

OPERATING SYSTEM: PC-DOS/MS-DOS

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reising, Ethington, Barnard & Perry

STREET: P.O. Box 4390

CITY: Troy

STATE: Michigan

COUNTRY: US

ZIP: 48099

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/370,156

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-307 (Mulford)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 160..1959
US-08-370-156-3

alignment_scores:
Quality: 14.00 Length: 14
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x US-08-370-156-3 ..

Align seg 1/1 to: US-08-370-156-3 from: 1 to: 3096

1 AlaGlupHeHisArgTrpSerTyrMetValHisTrpLys 14
|||||
2755 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 2796

seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-814-095-3

seq_documentation_block:

Sequence 3, Application US/08814095

Patent No. 6025183

GENERAL INFORMATION:

APPLICANT: Soreq, Hermona

APPLICANT: Zakut, Haim

APPLICANT: Shani, Moshe

TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR

OPERATING SYSTEM: PC-DOS/MS-DOS

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: KOHN & ASSOCIATES

STREET: 30500 No. 6025183thwestern Highway, Suite 410

CITY: Farmington Hills

STATE: Michigan

COUNTRY: U.S.

ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/814,095

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Montgomery, Ilene N.

REGISTRATION NUMBER: 38,972

REFERENCE/DOCKET NUMBER: 2391.00066

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3096 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Alternatively spliced Ache
; DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion
; DESCRIPTION: of Intron 4 (readthrough)"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..1959
; US-08-814-095-3

alignment_scores:
  Quality: 14.00 Length: 14
  Ratio: 1.000 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
  US-09-155-076-1 x US-08-814-095-3 ..
  Align seg 1/1 to: US-08-814-095-3 from: 1 to: 3096
  1 AlaGluPheHisArgTrrpSerSerTyrMetValHisIrrpLys 14
  |||||||||||||||||||||||||||||||||||||||||||
  2755 GCCGAGTCCACCGCTGGAGCTCTACATGCTGCACGTGAAG 2796

seq_name: /cgn2_5/ptodata/2/1na/6_COMB.seq:US-08-814-095-7
seq_documentation_block:
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including Ache
; DESCRIPTION: promoter, Ache gene and Ars gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
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; Patent No. 5820869
; GENERAL INFORMATION:
; APPLICANT: Wasmoen, Terri
; APPLICANT: Chu, Hsien-Jue
; APPLICANT: Chavez, Lloyd
; TITLE OF INVENTION: Recombinant Raccoon Pox Viruses and
; TITLE OF INVENTION: Their use as an Effective Vaccine Against Feline
; TITLE OF INVENTION: Immunodeficiency Virus Infection
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,090
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schaffer, Robert
; REGISTRATION NUMBER: 31,194
; REFERENCE/DOCKET NUMBER: 0632/0B170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)527-7700
; TELEFAX: (212)753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:03 ; Search time 10.69 seconds
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40.584 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 85661 seqs, 30989116 residues

Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SwissProt_38:*

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2	14	100.0	584	1 ACES_RABIT	Q29499 oryctolagus
3	14	100.0	614	1 ACES_HUMAN	P22303 homo sapien
4	14	100.0	614	1 ACES_MOUSE	P21836 mus musculu
5	14	100.0	614	1 ACES_RAT	P37136 rattus norv
6	9	64.3	767	1 ACES_CHICK	P36196 gallus gall
7	6	42.9	330	1 PMTL_SCHPO	P40999 schizosacch
8	5	35.7	235	1 HXD4_CHICK	P17278 gallus gall
9	5	35.7	236	1 HXD4_BRARE	O57374 brachydanio
10	5	35.7	250	1 HXD4_MOUSE	P10628 mus musculu
11	5	35.7	255	1 HXD4_HUMAN	P09016 homo sapien
12	5	35.7	282	1 YXJB_BACSV	P42313 bacillus su
13	5	35.7	408	1 YFYN_ECOLI	P46139 escherichia
14	5	35.7	427	1 PEPB_ECOLI	P37095 escherichia
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16	5	35.7	444	1 YODT_BACSV	O34662 bacillus su
17	5	35.7	486	1 PHOQ_ECOLI	P23837 escherichia
18	5	35.7	538	1 TPPI_MOUSE	O89023 mus musculu
19	5	35.7	603	1 CHLE_MOUSE	Q03311 mus musculu
20	5	35.7	619	1 YAL6_CHLPN	Q26633 chlamydia p
21	5	35.7	919	1 AMY_STRLI	Q05884 streptomyce
22	5	35.7	1018	1 YKZ6_CAEEL	P34333 caenorhabdi
23	5	35.7	1886	1 GP21_RAT	P11654 rattus norv
24	4	28.6	21	1 RL5_HALME	P50557 halobacteri
25	4	28.6	58	1 RL30_HAEIN	P44366 haemophilus
26	4	28.6	59	1 RL30_ACYKS	P46184 acyrthosiph
27	4	28.6	82	1 YHYD_ANACY	P16420 anabaena cy
28	4	28.6	95	1 FER1_DUNSA	P00239 dunaliella
29	4	28.6	97	1 NHPI_BABBO	P40632 babesia bov
30	4	28.6	101	1 CYAV_HAEIN	P1358 haemophilus
31	4	28.6	101	1 Y53_BPT3	P20327 bacterioph
32	4	28.6	106	1 CYAY_ECOLI	P27838 escherichia
33	4	28.6	106	1 FER_MYCSM	P00215 mycobacteri

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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36	4	28.6	108	1 KV6K_MOUSE	P04945 mus musculu
37	4	28.6	114	1 KEDA_ACTSL	P41249 actinomycet
38	4	28.6	118	1 ABBE_TRIAB	P81116 trimeresuru
39	4	28.6	123	1 ABA4_TRIAB	P81114 trimeresuru
40	4	28.6	125	1 ABA3_TRIAB	P81113 trimeresuru
41	4	28.6	125	1 BOTB_BOTJA	P22030 bothrops ja
42	4	28.6	126	1 TRBF_ECOLI	P15068 escherichia
43	4	28.6	130	1 GUN2_PRAE	P23666 persea amer
44	4	28.6	131	1 ABA1_TRIAB	P81111 trimeresuru
45	4	28.6	133	1 BOTA_BOTJA	P22029 bothrops ja

ALIGNMENTS

RESULT 1
ACES_BOVIN
ID ACES_BOVIN STANDARD; PRT; 583 AA.
AC P23795;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACETYLCHOLINESTERASE (EC 3.1.1.7).
GN ACHE.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
[1]
RN RP
RP SEQUENCE.
RC TISSUE=FETAL SERUM;
RX MEDLINE; 90306335.
RA Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
RA Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RA "Complete amino acid sequence of fetal bovine serum
RT acetylcholinesterase and its comparison in various regions with other
RT cholinesterases.";
RL FEBS Lett. 266:123-127(1990).
CC -|- FUNCTION: RAPIDLY HYDROLYSES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O -> CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR PIR; S10712; S10712.
DR HSP; P22303; 2CLJ.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle;
KW Neurotransmitter degradation; Glycoprotein.
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FT ACT_SITE 334 334 BY SIMILARITY.
FT ACT_SITE 447 447 BY SIMILARITY.
FT DISULFID 69 96 BY SIMILARITY.
FT DISULFID 257 272 BY SIMILARITY.
FT DISULFID 409 529 BY SIMILARITY.
FT DISULFID 580 580 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 61 61 POTENTIAL.
FT CARBOHYD 265 265 POTENTIAL.
FT CARBOHYD 350 350 POTENTIAL.
FT CARBOHYD 464 464 POTENTIAL.
FT CARBOHYD 541 541 POTENTIAL.
SQ SEQUENCE 583 AA; 64238 MW; 78655017E494279F CRC64;

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Best Local Similarity 100.0%; Pred. No. 9e-10;
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QY 1 AEFHRWSSYVHWK 14
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Db 555 AEFHRSSYVHWK 568

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RESULT 2
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AC Q29499;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (FRAGMENT).
GN ACHE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95010096.
RA Jbilo O., Lhermite Y., Toutant J., Chatonnet A.;
RT "Acetylcholinesterase and butyrylcholinesterase expression in adult
RT rabbit tissues and during development.";
RL Eur. J. Biochem. 225:115-124(1994).
CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CC CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CC CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
CC OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
CC ERYTHROCYTES.
CC -|- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
CC SOLUBLE FORM OF ACHE.
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC
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CC
CC EMBL; U05036; AAA53235.1; -
CC HSP; P22303; 2CLT.
CC PFAM; PF00135; Coesterase; 1.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
CC Neurotransmitter degradation; Glycoprotein.
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CC ACT_SITE 448 448
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Query Match 100.0%; Score 14; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 9e-10;
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DB 556 AEFHRSSYVHWK 569

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RESULT 3
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AC P22303;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
GN ACHE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91088577.
RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Ghatt A., Neville L.,
RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA Zakut H.;
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=ERYTHROCYTE;
RX MEDLINE; 89232136.
RA Chailani V., Derr D., Earles B., Schwell E., August T.;
RT "Purification and partial amino acid sequence analysis of human
RT erythrocyte acetylcholinesterase.";
RL FEBS Lett. 247:279-282(1989).
RN [3]
RP MUTAGENESIS OF CYS-611.
RX MEDLINE; 92084699.
RA Velan B., Grosfeld H., Kromman C., Leitner M., Gozes Y., Lazar A.,
RA Flashner Y., Marcus D., Cohen S., Shaferman A.;
RT "The effect of elimination of intersubunit disulfide bonds on the
RT activity, assembly, and secretion of recombinant human
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT mutant.";
RL J. Biol. Chem. 266:23977-23984(1991).
RN [4]
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX MEDLINE; 92388112.
RA Shaferman A., Kromman C., Flashner Y., Leitner M., Grosfeld H.,
RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT "Mutagenesis of human acetylcholinesterase. Identification of
RT residues involved in catalytic activity and in polypeptide folding.";
RL J. Biol. Chem. 267:17640-17648(1992).
RN [5]
RP VARIANT BLOOD GROUP YT(B).
RX MEDLINE; 93256075.
RA Bartels C.F., Zelinski T., Lockridge O.;
RT "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
RT accounts for YT blood group polymorphism.";
RL Am. J. Hum. Genet. 52:928-936(1993).
CC -|- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -|- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -|- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -|- POLYMORPHISM: ACHE IS RESPONSIBLE FOR THE YT BLOOD GROUP SYSTEM.
CC THE MOLECULAR BASIS OF THE YT(A)-YT(B)/YT(B)-YT2 BLOOD GROUP
CC ANTIGENS IS A SINGLE VARIATION IN POSITION 353; HIS-353
CC CORRESPONDS TO YT(A) AND THE RARE VARIANT WITH ASN-353 TO YT(B).
CC -|- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC

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DR EMBL; M55040; AAA68151.1; -.
DR PIR; S03959; S03959.
DR PIR; A39256; A39256.
DR PIR; 2CLJ; 04-MAR-98.
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DR CARBBANK; CCSD:32958; -.
DR CARBBANK; CCSD:35085; -.
DR CARBBANK; CCSD:36427; -.
DR SWISS-2DPAGE; P22303; HUMAN.
DR MIM; 100740; -.
DR MIM; 112100; -.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Polymorphism;
KW Blood group antigen; Alternative splicing; 3D-structure.
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FT ACT_SITE 365 365
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FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT VARIANT 353 353
FT MUTAGEN 234 234
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRSSSYMVHWK 14
Db 586 AEPHRSSSYMVHWK 599

RESULT 4
ID ACES_MOUSE STANDARD; PRT; 614 AA.
AC P21836;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
GN ACHE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 90380429.
RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution
of alternatively spliced mRNA species.";
RL Neuron 5:317-327(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX MEDLINE; 96067648.

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RA Bourne Y., Taylor P., Marchot P.;
RT "Acetylcholinesterase inhibition by fasciculin: crystal structure of
the complex.";
RL Cell 83:503-512(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE; 99115643.
RA Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT "Crystal structure of mouse acetylcholinesterase. A peripheral site-
occluding loop in a tetrameric assembly.";
RL J. Biol. Chem. 274:2963-2970(1999).
CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
CC -1- CATALYTIC ACTIVITY: ACETYLCHOLINE + H(2)O = CHOLINE + ACETATE.
CC -1- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT CATALYTIC SUBUNITS ARE ENCODED
BY ALTERNATIVELY SPLICED MENAS THAT ARISE FROM A SINGLE GENE.
CC THE T (ASYMMETRIC) FORM IS SHOWN HERE.
CC -1- TISSUE SPECIFICITY: PREDOMINATES IN MOST EXPRESSING TISSUES
EXCEPT ERYTHROCYTES WHERE A GLYCOPHOSPHOLIPID-ATTACHED FORM OF
ACHE PREDOMINATES.
CC -1- MISCELLANEOUS: SYNAPSES USUALLY CONTAIN ASYMMETRIC MOLECULES OF
CHOLINESTERASE, WITH A COLLAGEN-LIKE PART DISULFIDE-BONDED TO THE
CATALYTIC PART. A DIFFERENT, GLOBULAR TYPE OF CHOLINESTERASE
OCCURS ON THE OUTER SURFACES OF CELL MEMBRANES, INCLUDING THOSE OF
ERYTHROCYTES.
CC -1- MISCELLANEOUS: THIS IS THE CATALYTIC SUBUNIT OF AN ASYMMETRIC OR
SOLUBLE FORM OF ACHE.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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CC EMBL; X56518; CAA39867.1; -.
DR PIR; JH0314; JH0314.
DR FDB; IMAH; 03-APR-96.
DR FDB; IMAA; 20-APR-99.
DR MGD; MGI:87876; ACHE.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal;
KW Neurotransmitter degradation; Glycoprotein; Alternative splicing;
KW 3D-structure.
FT SIGNAL 1 31
FT CHAIN 32 614
FT ACT_SITE 234 234
FT ACT_SITE 365 365
FT ACT_SITE 478 478
FT DISULFID 100 127
FT DISULFID 288 303
FT DISULFID 440 560
FT DISULFID 611 611
FT CARBOHYD 296 296
FT CARBOHYD 381 381
FT CARBOHYD 495 495
FT SEQUENCE 614 AA; 68168 MW; 662512463C21172 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.4e-10;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEPHRSSSYMVHWK 14
Db 586 AEPHRSSSYMVHWK 599

```


SQ SEQUENCE 767 AA; 83020 MW; B1B3DF29C31F6062 CRC64;

Query Match 54.3%; Score 9; DB 1; Length 767;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EFRWSSYM 10
| | | | | | | | | |
Db 740 EFRWSSYM 748

RESULT 7
PMT1_SCHPO
ID PMT1_SCHPO STANDARD; PRT; 330 AA.
AC P40959; 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE DNA METHYLTRANSFERASE PMT1 (EC 2.1.1.-) (SPIM.SPOI) (M.SPOMI).
GN PMT1.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-972;
RX MEDLINE; 95166638.
RA Wilkinson C.R.M., Bartlett R., Nurse P., Bird A.P.;
RT "The fission yeast gene pmt1+ encodes a DNA methyltransferase
RT homologue.";
RL Nucleic Acids Res. 23:203-210(1995).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE; 96194447.
RA Pinarbasi E., Elliott J., Hornby D.P.;
RT "Activation of a yeast pseudo DNA methyltransferase by deletion of a
RT single amino acid.";
RL J. Mol. Biol. 257:804-813(1996).
CC -1- FUNCTION: DOES NOT HAVE A CYTOSINE-5 METHYLTRANSFERASE ACTIVITY
DUE TO THE INSERTION OF A SER RESIDUE BETWEEN THE PRO-CYS MOTIF
CC FOUND AT THE ACTIVE SITE OF C5 MTASES. WHEN THIS SERINE IS DELETED
CC IT BECOMES CATALYTICALLY ACTIVE AND RECOGNIZES AND METHYLATES THE
CC SEQUENCE CC[AT]GG.
CC -1- SIMILARITY: TO DNA (CYTOSINE-5)-METHYLTRANSFERASES (EC 2.1.1.37).
CC -----
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CC -----
CC EMBL; X82444; CAA57824.1; -;
CC REBASE; RB02888; M.Spomi.
CC PFAM; PF00145; DNA_methylase.2.
KW Transferase; Methyltransferase.
FT ACT_SITE 81 81 BY SIMILARITY.
SQ SEQUENCE 330 AA; 37976 MW; 50A7121FA7CF58A1 CRC64;

Query Match 42.9%; Score 6; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WSSYVM 11
| | | | | | | | | |
Db 208 WSSYVM 213

RESULT 8
HXD4_CHICK

ID HXD4_CHICK STANDARD; PRT; 235 AA.
AC P17278;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HOMEBOX PROTEIN HOX-D4 (CHOX-A).
GN HOXD4 OR HOXD-4 OR CHOX-A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90245562.
RA Sasaki H., Yokoyama E., Kuroiwa A.;
RT "Specific DNA binding of the two chicken Deformed family homeodomain
RT proteins, Chox-1.4 and Chox-a.";
RL Nucleic Acids Res. 18:1739-1747(1990).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC -1- FUNCTION: BINDS TO SITES IN THE 5'-FLANKING SEQUENCE OF ITS CODING
CC REGION WITH VARIOUS AFFINITIES. THE CONSENSUS SEQUENCES OF THE
CC HIGH AND LOW AFFINITY BINDING SITES ARE TAATGA(C/G) AND CTAATTTT.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC "DEFORMED" SUBFAMILY.
CC -----
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CC -----
CC EMBL; X52671; CAA36897.1; -;
CC EMBL; X52672; CAA36898.1; -;
CC PIR; S09256; S09256.
CC HSSP; P02833; ISAN.
CC TRANSFAC; T01753; -;
CC PFAM; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 123 128 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 144 203 HOMEBOX.
FT DOMAIN 212 217 SER-RICH.
SQ SEQUENCE 235 AA; 26662 MW; B7115D434033E4B5 CRC64;

Query Match 35.7%; Score 5; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SSYVM 11
| | | | | | | | | |
Db 4 SSYVM 8

RESULT 9
HXD4_BRARE
ID HXD4_BRARE STANDARD; PRT; 236 AA.
AC O57374;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HOMEBOX PROTEIN HOX-D4;
GN HOXD4.

OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prince V.E., Joly L., Ekker M., Ho R.K.;
 RT "Zebrafish box genes: genomic organization and modified colinear
 RT expression patterns in the trunk."
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
 CC "DEFORMED" SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; Y14548; CAA74883.1; ALT_INIT.
 DR ZFIN; ZDB-GENE-980526.214; HOXD4.
 DR PFAM; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00027; HOMEBOX_1; FALSE_NEG.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 125 130 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 146 205 HOMEBOX.
 FT SEQUENCE 236 AA; 27132 MW; AAE8C7F34F17B5E CRC64;
 SQ
 Query Match 35.7%; Score 5; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SSVYV 11
 Db 4 SSVYV 8
 RESULT 10
 ID HXD4_MOUSE STANDARD; PRT; 250 AA.
 AC P10628; P97451;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE HOMEBOX PROTEIN HOXD4 (HOXD-4.2) (HOXD-5.1).
 GN HOXD4 OR HOXD-4 OR HOXD-4.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88263027.
 RA Featherstone M.S., Baron A., Gaunt S.J., Mattei M.-G., Duboule D.;
 RT "Hox-5.1 defines a homeobox-containing gene locus on mouse chromosome
 RT 2."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4760-4764(1988).
 RN [2]
 RP REVISTONS.
 RX MEDLINE; 94173687.
 RA Rambaldi I., Kovacs E.N., Featherstone M.S.;
 RT "A proline-rich transcriptional activation domain in murine HOXD-4

RT (HOXD-4.2).";
 RL Nucleic Acids Res. 22:376-382(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV;
 RA Folberg A., Featherstone M.S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 175-198 FROM N.A.
 RX MEDLINE; 92212934.
 RA Nazari A., Kim Y., Nirenberg M.;
 RT "Hox-1.11 and Hox-4.9 homeobox genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2883-2887(1992).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
 CC "DEFORMED" SUBFAMILY.
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 CC -----
 DR EMBL; J03770; AAA20072.1; ALT_INIT.
 DR EMBL; M87804; AAA37851.1; -.
 DR EMBL; U77364; AAB41222.1; -.
 DR PIR; A36170; A36170.
 DR HSSP; P02833; 1SAN.
 DR TRANSFAC; T01752; -.
 DR MGD; MGI:96208; HOXD4.
 DR PFAM; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PROSITE; PS00027; ANTENNAPEDIA.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00032; ANTENNAPEDIA; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 131 136 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 152 211 HOMEBOX.
 FT DOMAIN 220 229 SER-RICH.
 FT CONFLICT 143 143 A -> V (IN REF. 3).
 FT SEQUENCE 250 AA; 27284 MW; 1057647C0A2665FF CRC64;
 SQ
 Query Match 35.7%; Score 5; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 SSVYV 11
 Db 4 SSVYV 8
 RESULT 11
 ID HXD4_HUMAN STANDARD; PRT; 255 AA.
 AC P09016;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1990 (Rel. 15, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HOMEBOX PROTEIN HOXD4 (HOXD-4B) (HOXD-5.1) (HMO.C13).
 GN HOXD4 OR HOXD4B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 90356367.
 RA Clanetti L., di Cristofaro A., Zappavigna V., Bottero L.,
 RA Boccini G., Testa U., Russo G., Boncinelli E., Peschle C.,
 RT "Molecular mechanisms underlying the expression of the human HOX-5.1
 RT gene.",
 RL Nucleic Acids Res. 18:4361-4368(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87090377.
 RA Mavilio F., Simeone A., Giampaolo A., Faiella A., Zappavigna V.,
 RA Acampora D., Polana G., Russo G., Peschle C., Boncinelli E.,
 RT "Differential and stage-related expression in embryonic tissues of a
 RT new human homeobox gene.",
 RL Nature 324:664-668(1986).
 RN [3]
 RP SEQUENCE OF 154-219 FROM N.A.
 RX MEDLINE; 90215236.
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaudino G., Stornaluo A., Cafiero M., Faiella A., Simeone A.,
 RT "Organization of human class I homeobox genes.",
 RL Genome 31:745-756(1989).
 CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
 CC "DEFORMED" SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; X17360; CAA35237.1; -;
 CC EMBL; X04706; CAA28411.1; -;
 CC PIR; S10985; WJHU4B.
 CC HSP; P02833; ISAN.
 CC TRANSFAC; T00376; -;
 CC MIM; 142981; -;
 CC PFAM; PF00046; homeobox; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC PRINTS; PR00025; ANTENNAPEDIA.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS00032; ANTENNAPEDIA; 1.
 CC PROSITE; PS00071; HOMEBOX_2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 KW Transcription regulation.
 FT DOMAIN 133 138 ANTP-TYPE HEXAPEPTIDE.
 FT DNA_BIND 154 213 HOMEBOX.
 FT DOMAIN 222 234 POLY-SER.
 FT CONFLICT 123 123 P -> S (IN REF. 2).
 FT CONFLICT 142 142 V -> A (IN REF. 2).
 FT SEQUENCE 255 AA; 27895 MW; 3920508CCCAF16FF CRC64;
 * SQ
 Query Match 35.7%; Score 5; DB 1; Length 255;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 SSMV 11
 Db 4 SSMV 8
 RESULT 12
 YXJB_BACSU
 ID YXJB_BACSU STANDARD; PRT; 282 AA.
 AC P42313;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL 31.5 KDA PROTEIN IN KATB 3'REGION.
 GN YXJB OR N151.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / BGSC1A1;
 RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO E.COLI RMA AND M.GRISORUBIDA MYRA.
 CC -----
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 CC -----
 CC EMBL; D83026; BAA11703.1; -;
 CC EMBL; Z99123; CAB15927.1; -;
 CC EMBL; Z99124; CAB15937.1; -;
 CC SUBTILIST; EG1151; YXJB.
 KW Hypothetical protein.
 SQ SEQUENCE 282 AA; 31473 MW; 35DE65D847D67E61 CRC64;
 Query Match 35.7%; Score 5; DB 1; Length 282;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHR 5
 Db 172 AEFHR 176
 RESULT 13
 YFIN_ECOLI
 ID YFIN_ECOLI STANDARD; PRT; 408 AA.
 AC P46139; F76598;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 46.0 KDA PROTEIN IN AROF-RPLS INTERGENIC REGION.
 GN YFIN.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE OF 330-408 FROM N.A.
 RX MEDLINE; 84057772.
 RA Byström A.S., Hjalmarsson K.J., Wikström P.M., Bjoerk G.R.;
 RT "The nucleotide sequence of an Escherichia coli operon containing
 RT genes for the tRNA(m⁶G)methyltransferase, the ribosomal proteins S16
 RT and t19 and a 21-K polypeptide.";
 RL EMBO J. 2:899-905(1983).
 RN [3]
 RP IDENTIFICATION
 RX MEDLINE; 96032851.
 RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
 RA Danchin A.;

RT "Detection of new genes in a bacterial genome using Markov models for
 RT three gene classes";
 RL Nucleic Acids Res. 23:3554-3562(1995).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (B.SUBTILIS)
 CC FAMILY
 CC -----
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 CC -----
 DR EMBL; AE000346; AAC75653.1; -;
 DR EMBL; X01818; -; NOT_ANNOTATED_CDS.
 DR ECOCENE; EG12880; YFIN.
 DR PFAM; PF00990; DUF9; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 113 133 POTENTIAL.
 FT TRANSMEM 155 175 POTENTIAL.
 SQ SEQUENCE 408 AA; 45989 MW; 720B6539EF43DB16 CRC64;

 Query Match 35.7%; Score 5; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHR 5
 Db 215 AEFHR 219

 RESULT 14
 ID PEPR_ECOLI STANDARD; PRT; 427 AA.
 AC P37095; Q47131; P76580; P76989; P76991;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PEPTIDASE B (EC 3.-.-.-).
 GN PEPR.
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 CC [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Suzuki H., Kim E., Yamamoto N., Hashimoto W., Yamamoto K., Kumagai H.;
 RT "Mapping, cloning, and DNA sequencing of pepr gene which encodes
 RT peptidase B of Escherichia coli K-12.";
 RL J. Ferment. Bioeng. 82:392-397(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
 RA Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K.,
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,
 RA Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,
 RA Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,

RA Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yamamoto Y., Iano M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC SEQUENCE OF 1-42 FROM N.A.
 RP STRAIN-K12;
 RX MEDLINE; 94131939.
 RA Kawula T.H., Lelivelt M.J.;
 RT "Mutations in a gene encoding a new Hsp70 suppress rapid DNA
 RT inversion and bgl activation, but not proU derepression, in hns-1
 RT mutant Escherichia coli.";
 RL J. Bacteriol. 176:610-619(1994).
 CC -!- CAPACITOR: ACTIVATED BY MANGANESE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M17; ALSO KNOWN AS THE
 CC CYTOSOL AMINOPEPTIDASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; D84499; BAA12689.1; -;
 DR EMBL; AE000339; AAC75576.1; ALT_INIT.
 DR EMBL; D90882; CAB22347.1; -;
 DR EMBL; D90883; CAB22357.1; -;
 DR EMBL; U01827; -; NOT_ANNOTATED_CDS.
 DR HSSP; P00727; ILAP.
 DR ECOCENE; EG12310; PEPR.
 DR PFAM; PF00883; Peptidase_M17; 1.
 DR PRINTS; PR00481; LAMNOPPTDASE..
 DR PROSITE; PS00631; CYTOSOL_AP; 1.
 KW Hydrolase; Manganese.
 FT METAL 195 195
 FT METAL 200 200 MANGANESE (2) (BY SIMILARITY).
 FT METAL 218 218 MANGANESE (1 AND 2) (BY SIMILARITY).
 FT METAL 277 277 MANGANESE (2) (BY SIMILARITY).
 FT METAL 279 279 MANGANESE (1 AND 2) (BY SIMILARITY).
 FT ACT_SITE 207 207 POTENTIAL.
 FT ACT_SITE 281 281 POTENTIAL.
 FT CONFLICT 155 155 Q -> P (IN REF. 1).
 FT CONFLICT 375 426 STAAGFLSHVENYQQGWLHDCSATYRKAPQWSAGATG.
 FT LGVRTIANLIT -> TERRASCRTLLRTISKACISTARRL
 FT TVKRLNSGLRALDVC (IN REF. 1).
 FT L -> P (IN REF. 3).
 SQ SEQUENCE 427 AA; 46180 MW; 8299E7D440F5732E CRC64;

 Query Match 35.7%; Score 5; DB 1; Length 427;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AEFHR 5
 Db 348 AEFHR 352

 RESULT 15
 ID NU4M_LOCOMI STANDARD; PRT; 444 AA.
 AC Q36424;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3).
 GN ND4.
 OS Locusta migratoria (Migratory locust).
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthoptera; Orthopteroidea; Caelifera;
 CC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.

```

RN  SEQUENCE FROM N.A.
RP  MEDLINE: 96139026.
RA  Flock P.K., Rowell C.H.F., Gellissen G.;
RT  "The sequence, organization, and evolution of the Locusta migratoria
RL  mitochondrial genome.";
RJ  J. Mol. Evol. 41:928-941(1995).
CC  -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X80245; CAA56534.1; -
DR  PFAM; PF00361; oxidored_g1; 1.
DR  PFAM; PF01059; oxidored_g5_N; 1.
KW  Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ  SEQUENCE 444 AA; 51135 MW; B2D8DEC2584921BA CRC64;

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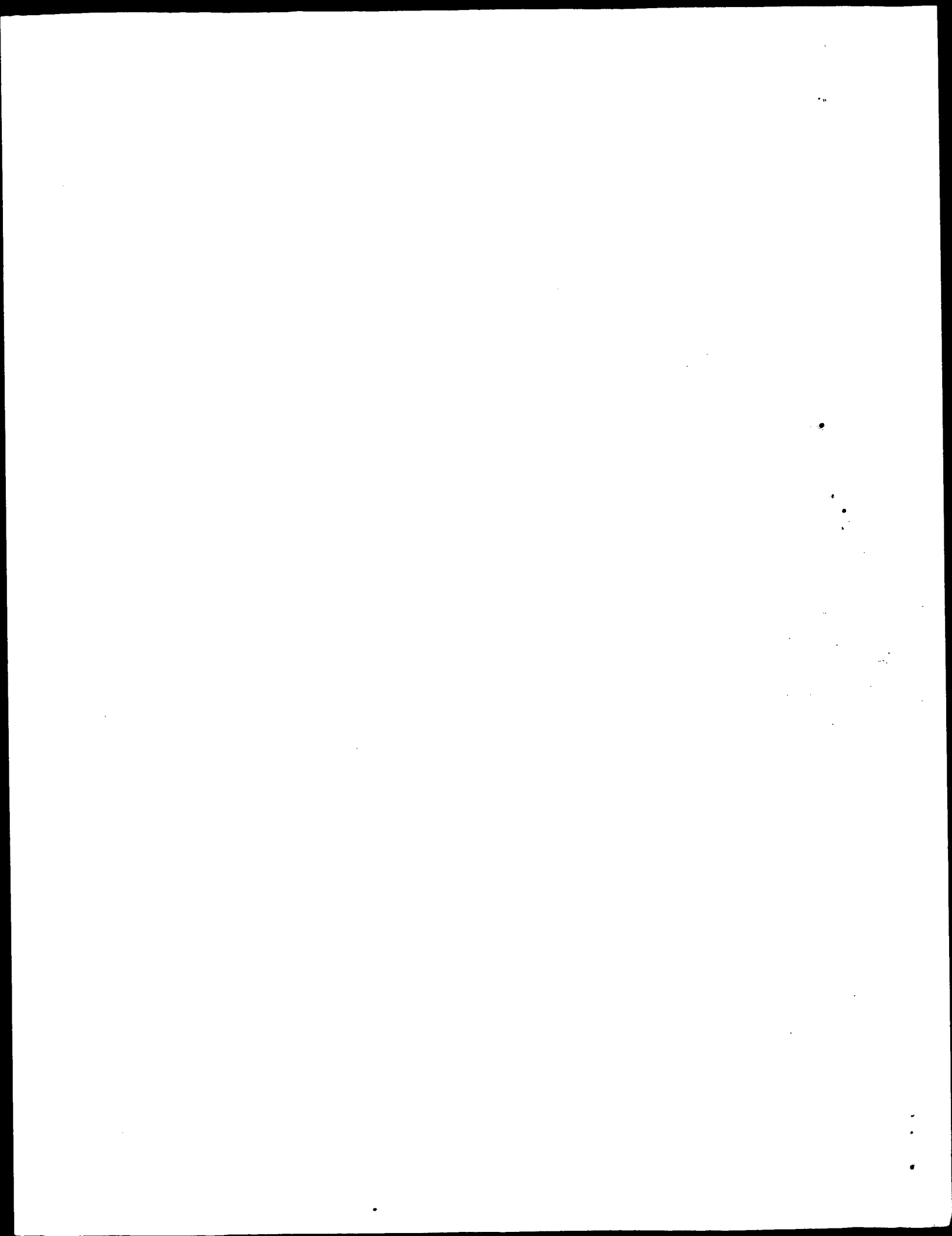
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Query Match      35.7%; Score 5; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 WSSYM 10
Db  376 WSSYM 380

```

Search completed: September 13, 2000, 02:27:53
Job time: 170 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:12 ; Search time 22.49 Seconds
(without alignments)
43.160 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSVMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	611	6	062763 felis silve
2	84	96.6	633	13	042275 electrophor
3	80	92.0	95	13	09w6y8 torpedo cal
4	70	80.5	95	13	073748 bungarus fa
5	56	64.4	602	6	062760 felis silve
6	56	64.4	602	6	062761 panchera ti
7	44	50.6	260	8	078318 arabidopsis
8	42	48.3	1788	4	060611 homo sapien
9	42	48.3	1788	4	060612 homo sapien
10	42	48.3	1792	6	046385 bos taurus
11	42	48.3	2214	4	095425 homo sapien
12	41	47.1	1323	11	062255 mus musculu
13	41	47.1	1687	10	09xgn9 oryza sativ
14	40.5	46.6	285	2	Q52970 rhizobium m
15	40.5	46.6	508	8	078332 perglaria
16	40.5	46.6	508	8	063177 plocosperma
17	40.5	46.6	511	8	078334 tylophora l
18	40.5	46.6	511	8	078335 vincetoxicu
19	40	46.0	183	2	Q57000 zymomonas m

20	40	46.0	351	12	072754
21	40	46.0	450	2	025000
22	40	46.0	517	8	09xpp6
23	40	46.0	1350	13	091929
24	39.5	45.4	469	2	073738
25	39.5	45.4	512	8	078333
26	39.5	45.4	542	10	064858
27	39.5	45.4	1057	3	09y8h1
28	39	44.8	100	10	023949
29	39	44.8	226	12	037049
30	39	44.8	226	12	037351
31	39	44.8	226	12	075004
32	39	44.8	226	12	072839
33	39	44.8	226	8	078312
34	39	44.8	260	8	078311
35	39	44.8	260	8	078319
36	39	44.8	260	8	078320
37	39	44.8	262	12	010441
38	39	44.8	441	5	015814
39	39	44.8	524	10	049650
40	39	44.8	526	10	049652
41	38.5	44.3	287	10	092504
42	38.5	44.3	318	5	091927
43	38.5	44.3	354	8	098848
44	38	43.7	65	13	098928
45	38	43.7	117	8	09xmn6

ALIGNMENTS

RESULT 1
062763 PRELIMINARY; PRT; 611 AA.
AC 062763;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE ACETYLCHOLINESTERASE COLLAGEN-TAILED OR GLOBULAR FORM PRECURSOR.
GN ACHE.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RA BARTLS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053485; AAC08995.1; -
DR HSSP; P22303; 2CLJ.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
SQ SEQUENCE 611 AA; 67298 MW; 172DEB16 CRC32;

Query Match 100.0%; Score 87; DB 6; Length 611;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEFHRWSSVMVHWK 14
|||||
DB 583 AEFHRWSSVMVHWK 596

RESULT 2
042275 PRELIMINARY; PRT; 633 AA.
ID 042275;
AC 042275;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE ACETYLCHOLINESTERASE CATALYTIC SUBUNIT PRECURSOR (EC 3.1.1.7).

OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Gymnotiformes;
OC Gymnotoidei; Electrophoridae; Electrophorus.
[1]
RP SEQUENCE FROM N.A.
RA SIMON S., MASSOULIE J.;
RL J. Biol. Chem. 0:0-0(1997).
DR EMBL; AF030422; AAB86606.1; -.
DR HSSP; P04058; IACL.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 2.
DR PRINTS; PR00878; CHOLNESTRASE.
KW Signal; Hydrolase. 23 POTENTIAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 633 POTENTIAL.
SQ SEQUENCE 633 AA; 71814 MW; 6D50AB05 CRC32;

Query Match 96.6%; Score 84; DB 13; Length 633;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AEFHRSWSSVMVHWK 14
| | | | | | | | | | | | | | | | | |
Db 605 AEFHRSWSSVMVHWK 618

RESULT 3
Q9W6Y8 PRELIMINARY; PRT; 95 AA.
ID Q9W6Y8
AC Q9W6Y8
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ACETYLCOLINESTERASE (FRAGMENT).
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Rajiformes; Torpedinoidei; Torpedinidae; Torpedo.
[1]
RP SEQUENCE FROM N.A.
RA MAULET Y., CAMP S., GIBNEY G., RACHINSKY T.L., ERSTROEM T.J.,
RA TAYLOR P.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X56517; CAB37951.1; -.
DR EMBL; X56516; CAB37951.1; JOINED.
FT NON_TER 1 1
SQ SEQUENCE 95 AA; 11752 MW; F7387712 CRC32;

Query Match 92.0%; Score 80; DB 13; Length 95;
Best Local Similarity 92.3%; Pred. No. 7.9e-06;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 EFRHRSWSSVMVHWK 14
| | | | | | | | | | | | | | | | | |
Db 68 EFRHRSWSSVMVHWK 80

RESULT 4
O73748 PRELIMINARY; PRT; 95 AA.
ID O73748
AC O73748
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ACETYLCOLINESTERASE (FRAGMENT).
OS Bungarus fasciatus (Banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Bungarinae;
OC Bungarus.
[1]

RP SEQUENCE FROM N.A.
RA COUSIN X., BON S., MASSOULIE J., BON C.;
RL J. Biol. Chem. 0:0-0(1998).
DR EMBL; AF045238; AAC16420.1; -.
DR HSSP; P21836; IMAH.
FT NON_TER 1 1
SQ SEQUENCE 95 AA; 11225 MW; 13280E02 CRC32;

Query Match 80.5%; Score 70; DB 13; Length 95;
Best Local Similarity 76.9%; Pred. No. 0.00029;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 EFRHRSWSSVMVHWK 14
| | | | | | | | | | | | | | | | | |
Db 68 EFRHRSWSSVMVHWK 80

RESULT 5
O62760 PRELIMINARY; PRT; 602 AA.
ID O62760
AC O62760
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE BUTYRYLCOLINESTERASE PRECURSOR.
GN BCHE.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY;
RA BARTLS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053483; AAC06261.1; -.
DR HSSP; P21836; IMAH.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
KW Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 602 BUTYRYLCOLINESTERASE.
SQ SEQUENCE 602 AA; 68328 MW; 27B133D7 CRC32;

Query Match 64.4%; Score 56; DB 6; Length 602;
Best Local Similarity 57.1%; Pred. No. 0.29;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 AEFHRSWSSVMVHWK 14
| | | | | | | | | | | | | | | | | |
Db 573 AGFYRWNNYMDWK 586

RESULT 6
O62761 PRELIMINARY; PRT; 602 AA.
ID O62761
AC O62761
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE BUTYRYLCOLINESTERASE PRECURSOR.
GN BCHE.
OS Panthera tigris tigris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY;
RA BARTLS C.F., XIE W.-H., MILLER-LINDHOLM A.K., LOCKRIDGE O.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF053484; AAC06262.1;
DR HSSP; P21836; IMAH.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
DR PFAM; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
KW SIGNAL.
FT SIGNAL. 1 28 POTENTIAL.
FT CHAIN 29 602 BUTYRYLCHOLINESTERASE.
SQ SEQUENCE 602 AA; 68290 MW; B019C09B CRC32;

Query Match 64.4%; Score 56; DB 6; Length 602;
Best Local Similarity 57.1%; Pred. No. 0.29;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
| :|:|:|:|:|
DB 573 AGFYRWNNYMDWK 586

RESULT 7
ID O78318 PRELIMINARY; PRT; 260 AA.
AC O78318;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE NADH DEHYDROGENASE SUBUNIT F (FRAGMENT).
GN NDHF.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA GALLOWAY G.L., MALMBERG R.L., PRICE R.A.;
RT "Phylogenetic utility of the nuclear gene arginine decarboxylase
RT within Brassicaceae.";
RL Mol. Biol. Evol. 0:0-0(1998).
DR EMBL; AF06454; AAC68593.1;
DR MENDEL; 30386; Arath; ndhf; 30386.
DR PFAM; PF01010; oxidored_g1_C; 1.
KW Chloroplast.
KW NON_TER 1
FT NON_TER 260 260
FT SEQUENCE 260 AA; 30565 MW; 916B2FFC CRC32;

Query Match 50.6%; Score 44; DB 8; Length 260;
Best Local Similarity 41.7%; Pred. No. 9.3;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 FHRWSSYVHWK 14
| :|:|:|:|:|
DB 192 FQWNSKRHW 203

RESULT 8
O60611 PRELIMINARY; PRT; 1788 AA.
ID O60611
AC O60611;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE SUPERVILLIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

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DE 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE SUPERVILLIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98044228.
RA PESTONJANASP K.N., POPE R.K., WULFKUHL J.D., LUNA E.J.;
RT "Supervillin (P05): A novel membrane-associated, F-actin-binding
RL protein in the villin/gelsolin superfamily.";
RL J. Cell Biol. 139:1255-1269(1997).
DR EMBL; AF025996; AAC48783.1; -.
DR HSSP; P02640; 1VII.
DR PFAM; PF00626; Gelsolin; 1.
SQ SEQUENCE 1792 AA; 200625 MW; 29AEB3CE CRC32;

Query Match 48.3%; Score 42; DB 6; Length 1792;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFHRWSSYVHWK 14
:|:|:|:|:|
Db 1352 QFHEGDYVVRWK 1364

RESULT 11
Q95425 PRELIMINARY; PRT; 2214 AA.
AC Q95425;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE ARCHVILLIN.
GN SVIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99058997.
RA POPE R.K., PESTONJANASP K.N., SMITH K.P., WULFKUHL J.D.,
RA STRASSEL C.P., LAWRENCE J.B., LUNA E.J.;
RT "Cloning, characterization, and chromosomal localization of human
RT supervillin (SVIL).";
RL Genomics 52:342-351(1998).
DR EMBL; AF109135; AAD14682.1; -.
DR HSSP; P02640; 1VII.
SQ SEQUENCE 2214 AA; 247704 MW; 0204DCB9 CRC32;

Query Match 48.3%; Score 42; DB 4; Length 2214;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFHRWSSYVHWK 14
:|:|:|:|:|
Db 1774 QFHEGDYVVRWK 1786

RESULT 12
Q62255 PRELIMINARY; PRT; 1323 AA.
AC Q62255;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE SPALT HOMOLOGUE (SPALT PROTEIN) (FRAGMENT).
GN SPALT OR MSAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96391179.
RA OTT T., KAESTNER K.H., MONAGHAN A.P., SCHUTZ G.;
RT "The mouse homolog of the region specific homeotic gene spalt of
RT Drosophila is expressed in the developing nervous system and in
RT mesoderm-derived structures.";
RL Mech. Dev. 56:117-128(1996).
DR EMBL; X97581; CAA66196.1; -.
DR HSSP; P07248; IARE.
DR MGD; MGI:109295; Spalt.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 9.
DR PFAM; PF00096; zf-C2H2; 10.
KW Zinc-finger; Metal-binding; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 1323 AA; 139070 MW; DAD82AAD CRC32;

Query Match 47.1%; Score 41; DB 11; Length 1323;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 AEFHRWSSYVHWK 14
:|:|:|:|:|
Db 29 AEFKWAQFLQHK 42

RESULT 13
Q9XGN9 PRELIMINARY; PRT; 1687 AA.
AC Q9XGN9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE SIMILAR TO SEC7 PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Oryza.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPONBARE;
RA SASAKI T., MATSUMOTO T., YAMAMOTO K.;
RT "Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 2, PAC
RT clone:PO437H03 (contig b).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000367; BAA82387.1; -.
SQ SEQUENCE 1687 AA; 187179 MW; 5E0FDF99 CRC32;

Query Match 47.1%; Score 41; DB 10; Length 1687;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 EFHRWSSYVHWK 12
:|:|:|:|:|
Db 1492 ETRHWSFYAEH 1502

RESULT 14
Q52970 PRELIMINARY; PRT; 285 AA.
AC Q52970;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE MODULATION GENES NOD8, NOD8 AND NODC.
OS Rhizobium meliloti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
RN [1]
RP SEQUENCE FROM N.A.

```



```

RX MEDLINE; 85087953.
RA TOEROEK I., KONDOROSI E., STEPROWSKI T., POSFAI J., KONDOROSI A.;
RT "Nucleotide sequence of Rhizobium meliloti nodulation genes.";
RL Nucleic Acids Res. 12:9509-9524(1984).
DR EMBL; X01649; CAA25807.1; -.
SQ SEQUENCE 285 AA; 32342 MW; 157B9F20 CRC32;

Query Match 46.6%; Score 40.5; DB 2; Length 285;
Best Local Similarity 56.2%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 2 EPHRWSSYM---VHWK 14
   | | | | | | | |
Db 82 ETTHWSSYMSLKVQWK 97

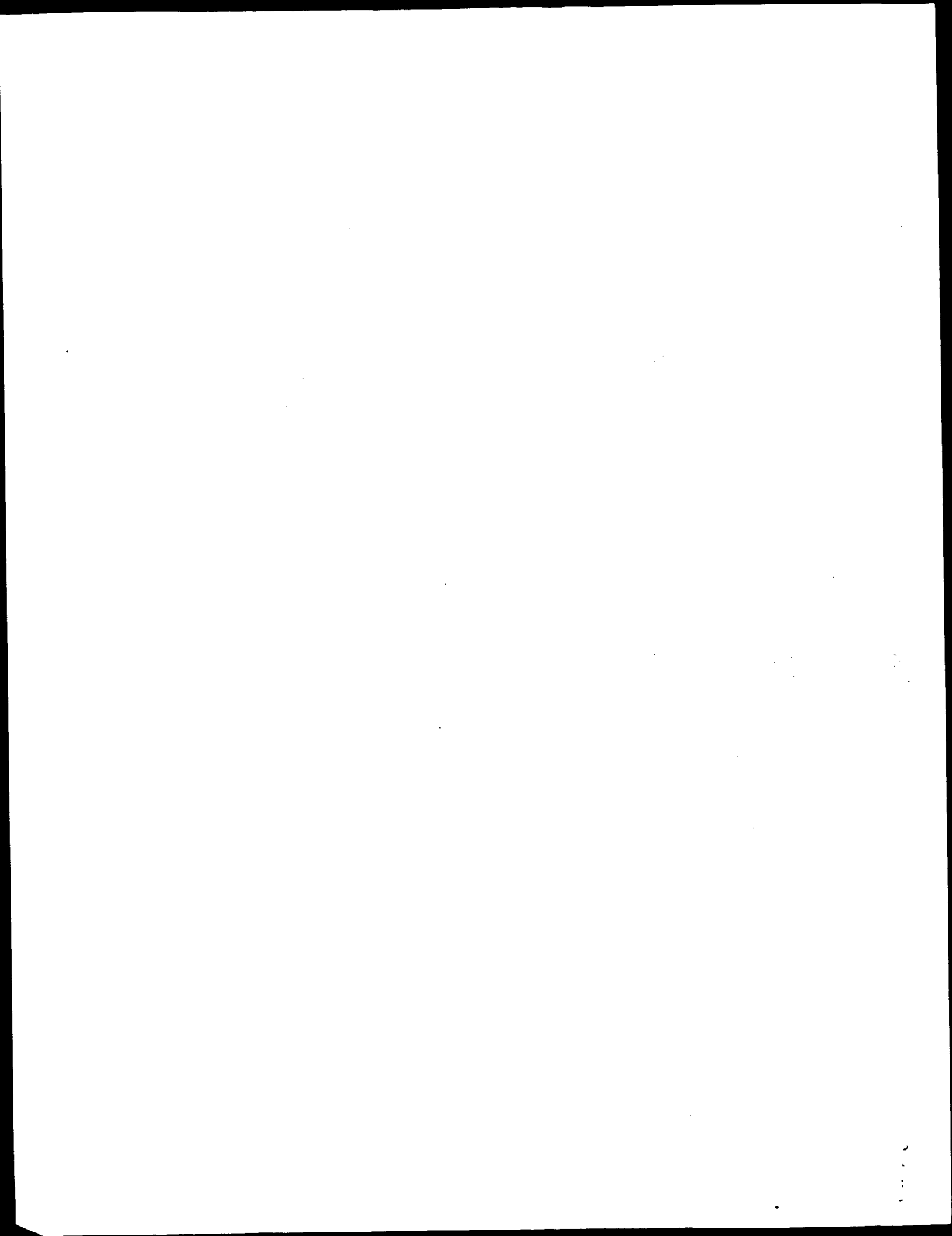
RESULT 15
O78332 PRELIMINARY; PRT; 508 AA.
AC O78332;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE MATUREASE (FRAGMENT).
GN YCF14 OR MATK.
OS Pergularia daemia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Gentianales; Asclepiadaceae;
OC Pergularia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98334575.
RA CIVEYREL L., LE THOMAS A., FERGUSON K., CHASE M.W.;
RT "Critical reexamination of palynological characters used to delimit
RT Asclepiadaceae in comparison to the molecular phylogeny obtained from
RT plastid matk sequences.";
RL Mol. Phylogenet. Evol. 9:517-527(1998).
DR EMBL; 298191; CAB10879.2; -.
DR MENDEL; 30397; Perda:ycf14:30397.
DR PFAM; PF01348; Intron_maturas2; 1.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 508 AA; 60145 MW; EC02C198 CRC32;

Query Match 46.6%; Score 40.5; DB 8; Length 508;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 4 HRWSSYMYH-WK 14
   : : | | | |
Db 299 NKWKSYLHFWQ 310

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Search completed: September 13, 2000, 02:24:09
 Job time: 177 sec



OM of: US-09-155-076-1 to: EST.* out_format : pfs

Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL=framet p2n.model -DEV=xlp
-O/cn2_1/USPTO.spool/US09155076/runat_29082000_092504_15735/app_query.fasta_1.144
-DB=EST -CFMT=fastap -SUFFIX=first -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09155076 -CGN1_1_1327 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-155-076-1

Query length: 14

Database: EST.*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 875.890000

score_list:

Sequence	Strd Orig	Zscore	Escore	Len	Documentation
gb_est50:N90761	+	87.00	254.64	248	N90761 zb22e03.s1 Soares fetal
gb_est52:T28280	+	87.00	254.42	254	T28280 EST35080 Human Embryo HC
gb_est25:A1764103	+	87.00	251.16	372	A1764103 UR-R-YO-acy-h-04-0-UI
gb_est48:F27586	+	87.00	250.76	372	F27586 HSPD15598 HM3 Homo sapie
gb_est14:AA933814	+	87.00	250.71	380	AA933814 0184009.s1 NCI_CGAP_KI
gb_est44:AA612795	+	87.00	250.61	384	AA612795 hh33a07.x1 NCI_CGAP_KI
gb_est14:AA998511	+	87.00	250.40	393	AA998511 UR-R-CO-le-h-11-0-UI
gb_est25:A1766812	+	87.00	250.35	395	A1766812 w189a12.x1 NCI_CGAP_KI
gb_est26:A1847791	+	87.00	250.35	395	A1847791 UR-M-AKI-aev-f-02-0-UI
gb_est24:A1360141	+	87.00	250.01	410	A1360141 Q83d10.x1 NCI_CGAP_KI
gb_est24:A190171	+	87.00	249.99	410	A190171 tx33a02.x1 NCI_CGAP_KI
gb_est7:AA401251	+	87.00	249.94	413	AA401251 zv66b01.s1 Soares tota
gb_est45:AA653940	+	87.00	248.15	496	AA653940 102878 MARC IBOV Bos t
gb_est1:AA030863	+	87.00	248.16	501	AA030863 mi45c07.r1 Soares mous
gb_est2:AA118440	+	87.00	247.92	514	AA118440 mo34s07.r1 Life Tech m
gb_est38:AA141312	+	87.00	247.76	523	AA141312 EST291353 Normalized r
gb_est19:A1325377	+	87.00	247.57	534	A1325377 mi45c07.y1 Soares mous
gb_est18:A1227851	+	87.00	247.47	540	A1227851 EST224546 Normalized r
gb_est19:A1323369	+	87.00	247.32	549	A1323369 mi45c07.x1 Soares mous
gb_est23:A1651494	+	83.00	239.15	364	A1651494 wb06d09.x1 NCI_CGAP_KI
gb_est4:AA271549	+	82.00	235.94	373	AA271549 vb74f09.r1 Soares mous
gb_est48:F34547	+	81.00	234.90	402	F34547 HSPD29467 HM3 Homo sapie
gb_est53:W15259	+	74.00	211.03	416	W15259 zb22e03.r1 Soares fetal
gb_est14:AA992576	+	71.00	196.46	764	AA992576 ot97e06.s1 Soares tota
gb_est43:AA531512	+	65.00	183.13	464	AA531512 UR-R-B01-aj1-h-01-0-UI
gb_est26:A1837078	+	64.00	183.51	322	A1837078 UR-M-AKO-ade-b-02-0-UI
gb_est24:A1695880	+	62.00	172.63	548	A1695880 ts87b04.x1 NCI_CGAP_KI
gb_est7:AA443431	+	62.00	172.00	587	AA443431 x294b01.r1 Soares tota
gb_est9:AA555331	+	62.00	170.13	719	AA555331 hk79h09.s1 NCI_CGAP_KI
gb_est13:AA885311	+	62.00	169.81	744	AA885311 al59f06.s1 Soares_NFL
gb_est13:A1015613	+	62.00	169.77	747	A1015613 ov29f06.x1 Soares test
gb_est25:A1829578	+	62.00	169.65	757	A1829578 wf28f01.x1 Soares_NFL
gb_est6:AA346027	+	57.00	163.19	302	AA346027 EST52141 Greater oment
gb_gss11:A0811907	+	56.00	156.71	441	A0811907 HS:5251.A2.C04_Sp6E_RP
gb_gss7:A0506219	+	53.00	147.02	477	A0506219 RPI:11-313B21.TU RPI
gb_est23:A1575368	+	52.00	146.91	349	A1575368 wb9e05.x1 NCI_CGAP_KI
gb_gss9:AQ724600	+	52.00	142.45	566	AQ724600 HS_5387.A2.H01.T7A RPI
gb_gss9:AQ633028	+	52.00	140.80	677	AQ633028 RPI:11-473N10.TV RPI
gb_gss18:CNS003MU	+	52.00	137.49	969	AL064706 Drosophila melanogaster
gb_gss18:CNS00CIS	+	52.00	137.33	986	AL059131 Drosophila melanogaster
gb_gss18:CNS00358	+	52.00	136.47	1083	AL065001 Drosophila melanogaster

gb_gss18:CNS00358 - 52.00 136.32 91.71 1101 ! AL064600 Drosophila melanogaster
gb_gss18:CNS00G7G - 52.00 136.32 91.71 1101 ! AL071732 Drosophila melanogaster
gb_gss18:CNS00LOD - 52.00 136.32 91.71 1101 ! AL068620 Drosophila melanogaster
gb_est5:AA318711 + 51.00 143.79 35.16 354 ! AA318711 EST20881 Adrenai ci

seq_name: gb_est50:N90761

seq_documentation_block:
LOCUS N90761 248 bp mRNA 03-APR-1996
DEFINITION zb22e03.s1 Soares fetal_lung NBHL19W Homo sapiens cDNA clone
IMAGE:302812 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION N90761
VERSION N90761.1 GI:1444088
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 248)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlff, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The Washu-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT On Dec 30, 1997 this sequence version replaced gi:905921.
Contact: Wilson RK
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

FEATURES

source

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="GB:1247744"

/db_xref="taxon:9606"

/clone="IMAGE:302812"

/clone_lib="Soares fetal_lung_NBHL19W"

/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-GCTTACCAATGATGAGGAGCGCGCAATTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NBHL19W."

BASE COUNT 47 a 89 c 57 g 47 t 8 others

ORIGIN

alignment_scores:

Quality: 87.00 Length: 14

Ratio: 6.214 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x N90761

Align seg 1/1 to: N90761 from: 1 to: 248

1 AlagluPheHisArgTrpSerSeryrMetValHisTrpLys 14
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 11 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 52

seq_name: gb_est52:T28280

seq_documentation_block: 254 bp mRNA EST 06-SEP-1995
 LOCUS T28280 Human Embryo Homo sapiens cDNA 5' end similar to
 DEFINITION acetylcholinesterase (HT:518), mRNA sequence.
 ACCESSION T28280
 VERSION T28280.1 GI:610378
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 254)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N., Kirtness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
 Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S.,
 Kelley,J.M., Klink,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
 Merrick,J.M., Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T.,
 Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
 Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
 Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A.,
 Coleman,T.A., Collins,E.J., Dimke,D., Feng,P., Ferrie,A.,
 Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
 Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
 Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
 Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
 Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns
 Based Upon 83 Million Basepairs of cDNA Sequence
 Nature 377, 3-174 (1995)
 JOURNAL Nature 377, 3-174 (1995)
 MEDLINE 96026280
 COMMENT On May 10, 1995 this sequence version replaced gi:805490.
 Other_ESTs: T2820776
 Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org)
 Insert Length: 1145 Std Error: 0.00
 Seq primer: M13 Reverse
 High quality sequence stop: 187.
 Location/Qualifiers
 1. .254
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):101797"
 /db_xref="taxon:9606"
 /clone_lib="Human Embryo"
 /tissue_type="embryo"
 45 a 89 c 78 g 41 t 1 others

alignment_scores:
 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-155-076-1 x T28280

Align seg 1/1 to: T28280 from: 1 to: 254

1 AlagluPheHisArgTrpSerSeryrMetValHisTrpLys 14
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 138 GCGAGTTCACCGCTGGAGCTCCTACATGGTGCACCTGGAAG 179

seq_name: gb_est25:AI764103

seq_documentation_block: 362 bp mRNA EST 25-JUN-1999
 LOCUS AI764103
 DEFINITION UI-R-YO-acy-h-04-0-UI-s1 UI-R-YO Rattus norvegicus cDNA clone
 UI-R-YO-acy-h-04-0-UI 3', mRNA sequence.
 ACCESSION AI764103
 VERSION AI764103.1 GI:5210038
 KEYWORDS EST.
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 362)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dt track served to verify it as a clone from the
 normalized Eye library cDNA Library Preparation: M.B. Soares Lab
 clone distribution: clones will be available through Research
 Genetics (www.resgen.com) The following repetitive elements were
 found in this cDNA sequence: 1-30, >POLY_A*Simple_repeat
 Seq primer: M13 Forward
 POLYA=Yes.
 Location/Qualifiers
 1. .362
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-YO-acy-h-04-0-UI"
 /clone_lib="UI-R-YO"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-YO
 library is a subtracted library derived from an
 individually-tagged normalized whole-eye (minus the lens)
 library. The driver for the subtraction consisted of a
 pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-E0,
 UI-R-E1, UI-R-CO, and UI-R-CI). The tag is a string of
 3-5 nucleotides present between the Not I site and the
 oligo-dt track which allows identification of the library
 of origin of a clone within the mixture. The subtracted
 library (UI-R-YO) was constructed as follows: PCR
 amplified cDNA inserts from previous library clones from
 which 3' ESTs had been derived were used as a driver in a
 hybridization with the normalized whole-eye library in
 the form of single-stranded circles. The remaining
 single-stranded circles (subtracted library) was purified
 by hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-YO

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 Source

library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 8: 791-806, 1996); TAG_L1IB-UI-R-Y0; TAG_TISSUE-Eye; TAG_SEQ-CATNG"

BASE COUNT
ORIGIN

71 a 87 c 116 g 88 t

alignment_scores:

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AI764103/rev ..

Align seg 1/1 to reverse of: AI764103 from: 1 to: 362

1 AlaGlupHeHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
340 GCCGAGTTCCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 299

seq_name: gb_est48:F27586

seq_documentation_block:

LOCUS F27586 378 bp mRNA EST 13-MAY-1999
DEFINITION HSPDI5598 HM3 Homo sapiens cDNA clone s4000002G06, mRNA sequence.
ACCESSION F27586
VERSION F27586.1 GI:4813212
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 378)
Pandolfo, D., Topppo, S., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,
Lanfranchi, G., Trevisan, S., Scarso, S. and Valle, G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)

JOURNAL

MEDLINE

COMMENT

On Jul 7, 1999 this sequence version replaced gi:5410190.

Contact: Valle G.

CRIBI Biotechnology Centre

University of Padua

Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at

http://group.bio.unipad.it.

FEATURES

source

Location/Qualifiers

1..378

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="s4000002G06"

/clone.lib="HM3"

/sex="female"

/tissue_type="pectoral muscle (after mastectomy)"

/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;

Site 2: NotI; The library was constructed by G.

Lanfranchi. This library is not subtracted nor normalized.

The first strand cDNA was primed with a biotinylated

oligo-dT-NotI primer

(5'-biotin-AACCCGCTCAGCGCGCTTTTTTTTTTTTTTTT-3'). The

ds cDNA was sonicated and size-selected in the range

350-550 bp. The 3' specific fragments were selected by

streptavidin coated magnetic beads, ligated to

non-palindromic BstXI adapters, NotI digested and

directionally cloned into BstXI-NotI cut pcDNAII vector."

BASE COUNT

ORIGIN

65 a 147 c 102 g 64 t

alignment_scores:

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AA933814

Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x F27586 ..

Align seg 1/1 to: F27586 from: 1 to: 378

1 AlaGlupHeHisArgTrpSerSerTyrMetValHisTrpLys 14
|||||
115 GCCGAGTTCCACCGCTGGAGCTCTACATGGTGCACCTGGAAG 156

seq_name: gb_est14:AA933814

seq_documentation_block:

LOCUS AA933814 380 bp mRNA EST 26-AUG-1998
DEFINITION O184b09.s1 NCI-CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1536281 3',
similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, MRNA
sequence.

ACCESSION AA933814

VERSION AA933814.1 GI:3090082

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 11, 1998 this sequence version replaced gi:2873131.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Sequencing by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 437 Std Error: 0.00

Seq primer: -40m13 fwd. RT from Amersham.

FEATURES

source

Location/Qualifiers

1..380

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1536281"

/clone.lib="NCI-CGAP_K1d5"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT73b-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(gt) primer [5'

AACGTGCAAGAAATCGCGCGCAATATTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo.

65 a 150 c 101 g 64 t

alignment_scores:

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Wed Sep 13 08:11:33 2000

Align seg 1/1 to: AA933814 from: 1 to: 380

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 115 GCCGAGTTCACCGCTGGAGCTCCTACATGTCGACTGGAAG 156

seq_name: gb_est44:AW612795

seq_documentation_block: 384 bp mRNA EST 23-MAR-2000
 LOCUS AW612795
 DEFINITION hh33a07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2958884 3'
 similar to contains PTR5.t3 PTR5 repetitive element ;, mRNA
 sequence.
 ACCESSION AW612795
 VERSION AW612795.1 GI:7317981
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 384)
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 image.lnl.gov/image/html/iresources.shtml

Possible reversed clone: polyT not found
 Seq primer: -400P from Gibco.

FEATURES
 source
 1..384
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2958884"
 /clone_lib="NCI_CGAP_Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI_CGAP_Lu5 was prepared, and ss circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (clonoids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo.
 66 a 154 c 96 g 68 t

BASE COUNT
 ORIGIN

alignment_scores:
 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AW612795 ..

Align seg 1/1 to: AW612795 from: 1 to: 384

1 AlagluPheHisArgTrpSerTyrMetValHisTrpLys 14
 115 GCCGAGTTCACCGCTGGAGCTCCTACATGTCGACTGGAAG 156

88 GCCGAGTTCACCGCTGGAGCTCCTACATGTCGACTGGAAG 129

seq_name: gb_est14:AA998511

seq_documentation_block: 393 bp mRNA EST 04-JUL-1999
 LOCUS AA998511
 DEFINITION UI-R-CO-ie-h-11-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone
 UI-R-CO-ie-h-11-0-UI.3', mRNA sequence.
 ACCESSION AA998511
 VERSION AA998511.1 GI:4290364
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 393)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 COMMENT On Jun 5, 1998 this sequence version replaced gi:3189162.
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565

Email: mscoares@blue.weeg.uiowa.edu
 The sequence tag present in the cDNA between the NotI site and the
 oligo-dt track served to identify it as a clone from the normalized
 adult Brain Library. cDNA Library Preparation: M. Fatima Bonaldo,
 Ph.D. Clone distribution: clones will be available through Research
 Genetics This clone is also available through the I.M.A.G.E.
 Consortium at LINL (info@image.lnl.gov). IMAGE ID=1774140
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 source

1..393
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CO-ie-h-11-0-UI"
 /clone_lib="UI-R-CO"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO
 library is a subtracted library derived from the UI-R-Al
 and UI-R-E1 libraries. The UI-R-Al library consisted of a
 mixture of individually tagged normalized libraries, liver,
 kidney, heart, spleen, ovary, and muscle. The UI-R-E1
 library consisted of a mixture of individually tagged
 normalized libraries constructed from 8, 12 and 18-day
 embryo. The tag is a string of 3-5 nucleotides present
 between the Not I site and the oligo-dt track which
 allows identification of the library of origin of a clone
 within the mixture. The subtracted library (UI-R-CO) was
 constructed as follows: PCR amplified cDNA inserts from a
 pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had
 been derived was used as a driver in a hybridization with
 the pooled UI-R-Al and UI-R-E1 library in the form of
 single-stranded circles. The remaining single-stranded
 circles (subtracted library) was purified by
 hydroxyapatite column chromatography, converted to
 double-stranded circles and electroporated into DH10B
 bacteria (Life Technologies) to generate the UI-R-CO
 library. This procedure has been previously described
 (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
 1996)"

BASE COUNT 80 a 92 c 130 g 91 t

ORIGIN

alignment_scores:
 Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AA998511/rev ..
 Align seg 1/1 to reverse of: AA998511 from: 1 to: 393

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14

327 GCCGAGTCCACCGCTGAGCTCTACATGTCGACTGGAG 286

seq_name: gb_est25:AI766812

seq_documentation_block:
 LOCUS AI766812 395 bp mRNA EST 21-DEC-1999
 DEFINITION w189a12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400478 3'
 similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR (HUMAN);, mRNA
 sequence.

ACCESSION AI766812
 VERSION AI766812.1 GI:5233321

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 395)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Apr 7, 1998 this sequence version replaced gi:3034669.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbrrp/image/image.html

Insert length: 442 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. .395

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2400478"

/clone_lib="NCI_CGAP_Kid12"

/tissue_type="2 pooled tumors (clear cell type)"

/lab_host="DH10B"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid5 was

prepared, and ss circles were made in vitro. Following HAP

purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs

from a pool of 5,000 clones made from the same library

(clones 1323912-1325831, 1471368-1472903 and

1492104-1493255). Subtraction by Bento Soares and M.

Fatima Bonaldo.

BASE COUNT

64 a 155 c 107 g 69 t

ORIGIN

alignment_scores:

Quality: 87.00 Length: 14
 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AI766812 ..

Align seg 1/1 to: AI766812 from: 1 to: 395

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
 |||||
 119 GCCGAGTCCACCGCTGAGCTCTACATGTCGACTGGAG 160

seq_name: gb_est26:AI847791

seq_documentation_block:

LOCUS AI847791 395 bp mRNA EST 15-JUL-1999
 DEFINITION UI-M-AK1-aev-f-02-0-UI.s1 NIH_BMAP_MHY_N Mus musculus cDNA clone
 UI-M-AK1-aev-f-02-0-UI 3', mRNA sequence.

ACCESSION AI847791

VERSION AI847791.1 GI:5491697

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 395)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

On Apr 7, 1998 this sequence version replaced gi:3035605.

Contact: Chan, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: m5t@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

normalized hypothalamus library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: NIH BMAP cDNA clones will be made

available by the means that is soon to be determined. When NIH

determines the means for distribution of the BMAP cDNA clones, this

record will be updated accordingly when that means is determined.

Seq primer: M13 Forward

PolyA-Yes.

Location/Qualifiers

1. .395

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UI-M-AK1-aev-f-02-0-UI"

/clone_lib="NIH_BMAP_MHY_N"

/dev_stage="27-32 days"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; The

NIH_BMAP_MHY_N library is a normalized library constructed

from mouse hypothalamus. The tag is a string of 5

nucleotides present between the Not I site and the

oligo-dT track. The library was constructed as described

by Bonaldo, Lennon and Soares, Genome Research 6:

791-806, 1996. Tissue provided by Ms. Annie Novakovich,

Zivic-Miller Laboratories.; TAG_LIB=NIH_BMAP_MHY_N;

TAG_TISSUE=hypothalamus; TAG_SEQ=CGTA

BASE COUNT

78 a 91 c 137 g 89 t

ORIGIN

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_scores:

US-09-155-076-1 x AI360141 ..

Align seg 1/1 to reverse of: AI847791 from: 1 to: 395

1 AlaGlupHeHisArgTrpSerSerTyrMetValHisTrpLys 14

119 GCGAGTTCACCGCTGGAGCTCTACATGGTGCACGGAAG 288

seq_name: gb_est19:AI360141

seq_documentation_block: 410 bp mRNA EST 16-FEB-1999

LOCUS qy83d10.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018611 3'

DEFINITION qy83d10.x1 NCI-CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018611 3'

(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI360141

VERSION AI360141.1 GI:4111762

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.

TITLE 1 (bases 1 to 410)

JOURNAL NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

On Jun 22, 1998 this sequence version replaced gi:3247207.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 440 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. 410

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2018611"

/clone_lib="NCI-CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site: 1; Site: 2; Eco RI; lsc

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAAGTGGGCGGCGCATAGTTTCTTTTCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 64 a 163 c 113 g 69 t 1 others

ORIGIN

alignment_scores:

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-1 x AI360141 ..

Align seg 1/1 to: AI360141 from: 1 to: 410

1 AlaGlupHeHisArgTrpSerSerTyrMetValHisTrpLys 14

119 GCGAGTTCACCGCTGGAGCTCTACATGGTGCACGGAAG 160

seq_name: gb_est24:AI690171

seq_documentation_block: 411 bp mRNA EST 16-DEC-1999

LOCUS AI690171

DEFINITION tx33a02.x1 NCI-CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271338 3'

similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR

(HUMAN); contains PTR5.b2 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI690171

VERSION AI690171.1 GI:4901465

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.

TITLE 1 (bases 1 to 411)

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2286587.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 458 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers

1. 411

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2271338"

/clone_lib="NCI-CGAP_Lu24"

/tissue_type="carcinoid"

/lab_host="DH10B"

/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Plasmid DNA from the normalized

library NCI-CGAP_Lu5 was prepared, and ss circles were

made in vitro. Following HAP purification, this DNA was

used as tracer in a subtractive hybridization reaction.

The driver was PCR-amplified cDNAs from a pool of 5,000

clones made from the same library (cloneIDs

1414920-1417991 and 1520904-1522439). Subtraction by Bento

Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 162 c 113 g 70 t

ORIGIN

alignment_scores:

Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:


```

US-09-155-076-1 x AI690171
Align seg 1/1 to: AI690171 from: 1 to: 411

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||
119 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 160

seq_name: gb_est7:AA401251

seq_documentation_block:
LOCUS AA401251 413 bp mRNA EST 16-MAY-1997
DEFINITION zv56b01.s1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:758569 3' similar to gb:M55040 ACETYLCHOLINESTERASE PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA401251
VERSION AA401251.1 GI:2055140
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 413)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washu-Merck EST Project 1997
Unpublished (1997)
JOURNAL On Jan 17, 1998 this sequence version replaced gi:2044207.
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -43ml3 fwd. ET from Amerisham.
FEATURES
Location/Qualifiers
source
1..413
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758569"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAACTGAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 68 a 163 c 111 g 71 t
ORIGIN

alignment_scores:
Quality: 87.00 Length: 14
Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000

alignment_block:
US-09-155-076-1 x AA401251
Align seg 1/1 to: AA401251 from: 1 to: 413

1 AlaGluPheHisArgTrpSerTyrMetValHisTrpLys 14
|||||
186 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 227

seq_name: gb_est1:AA030863

seq_documentation_block:
LOCUS AA030863 501 bp mRNA EST 21-AUG-1996
DEFINITION mi45c07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
clone IMAGE:466476 5' similar to gb:M55040 ACETYLCHOLINESTERASE
PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase
(MOUSE); mRNA sequence.

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|||||
118 GCCGAGTTCACCGCTGGAGCTCCTACATGGTGCACTGGAAG 159

seq_name: gb_est45:AW653940

```

```

seq_documentation_block:
LOCUS AW653940 496 bp mRNA EST 05-APR-2000
DEFINITION 102878 MARC LBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW653940
VERSION AW653940.1 GI:7419766
KEYWORDS EST.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 496)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
JOURNAL Contact: Smith TPL
COMMENT USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCGCCAGTCACGACG
Plate: 112 row: B column: 5
Seq primer: ATTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
source
1..496
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC LBOV"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site 1: XbaI; Site 2: XhoI;
Library made from pooled tissue from lymph node, ovary,
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alignment_scores:
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Ratio: 6.214 Gaps: 0
Percent Similarity: 100.000

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seq_name: gb_est1:AA030863

seq_documentation_block:
LOCUS AA030863 501 bp mRNA EST 21-AUG-1996
DEFINITION mi45c07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
clone IMAGE:466476 5' similar to gb:M55040 ACETYLCHOLINESTERASE
PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for acetylcholinesterase
(MOUSE); mRNA sequence.

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ACCESSION      AA030863
VERSION        AA030863.1  GI:1500851
KEYWORDS      EST.
SOURCE        Mus musculus
ORGANISM      house mouse.

REFERENCE
AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
              Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
              Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
              Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
              Waterston,R.

TITLE        The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
              WashU-HMI Mouse EST Project
              Washington University School of MedicineP
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              MGI:280292
              Seq primer: -28M13 rev2 from Amersham
              High quality sequence stop: 168.
              Location/Qualifiers
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                TGTTACCAATCTGAAGTGGAGCGCGCGAAATTTTTTTTTTTTTTTTTT
                T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                14.5dpc embryos [total RNA provided by Minoru KO, Wayne
                State Univ, from 2 l; double-stranded cDNA was ligated to
                Eco RI adaptors (Pharmacia), digested with Not I and
                cloned into the Not I and Eco RI sites of the modified
                pT7T3 vector. Library went through one round of
                normalization, and was constructed by Bento Soares and
                M.Fatima Bonaldo."
                M.Fatima Bonaldo."

BASE COUNT    97 a 163 c 138 g 103 t
ORIGIN

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  Percent Similarity: 100.000  Percent Identity: 100.000

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seq_name: gb_est2:AA118440

seq_documentation_block:
LOCUS      AA118440
DEFINITION mo34a07.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus

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CDNA clone IMAGE:555444 5' similar to gb:M55040
 ACETYLCHOLINESTERASE PRECURSOR (HUMAN); gb:X56518 Mouse mRNA for
 acetylcholinesterase (MOUSE);, mRNA sequence.

ACCESSION AA118440
VERSION AA118440.1 GI:1676072
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM house mouse.

REFERENCE
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:336236
 Seq primer: -28M13 rev1 from Amersham
 High quality sequence stop: 234.
 Location/Qualifiers
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BASE COUNT 89 a 180 c 130 g 115 t
ORIGIN

alignment_scores
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 Ratio: 6.214 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block
US-09-155-076-1 x AA118440 ..

Align seg 1/1 to: AA118440 from: 1 to: 514

1 AlaGluPheHisArgTrpSerSerTyrMetValHisTrpLys 14
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202 GCCGAGTTCACCGCTGGAGCTCTACATGGTGCCTGGAAG 243

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:26 ; Search time 14.59 Seconds
(without alignments)
16.811 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	1	US-08-302-808-10
2	16	100.0	16	2	US-08-986-948-10
3	16	100.0	21	2	US-08-659-984A-18
4	16	100.0	27	1	US-08-141-324-11
5	16	100.0	27	1	US-08-141-324-12
6	16	100.0	27	1	US-08-541-902-11
7	16	100.0	27	1	US-08-541-902-12
8	16	100.0	28	1	US-08-346-849-4
9	16	100.0	28	1	US-08-302-808-7
10	16	100.0	28	2	US-08-609-090-2
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12	16	100.0	28	2	US-08-293-284A-4
13	16	100.0	28	2	US-08-461-216-2
14	16	100.0	30	2	US-08-609-090-3
15	16	100.0	33	2	US-08-609-090-4
16	16	100.0	33	2	US-08-659-984A-16
17	16	100.0	35	2	US-08-304-585-6
18	16	100.0	35	2	US-08-612-785B-15
19	16	100.0	35	2	US-08-612-785B-38
20	16	100.0	36	2	US-08-609-090-6
21	16	100.0	38	1	US-08-302-808-1
22	16	100.0	38	2	US-07-737-371E-68
23	16	100.0	38	2	US-08-986-948-1
24	16	100.0	39	1	US-08-302-808-2
25	16	100.0	39	2	US-08-609-090-7
26	16	100.0	39	2	US-08-682-245A-1
27	16	100.0	39	2	US-08-986-948-2
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31 16 100.0 40 1 US-08-304-585-1 Sequence 1, Appli
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35 16 100.0 40 2 US-08-609-090-8 Sequence 69, Appli
36 16 100.0 40 2 US-08-682-245A-2 Sequence 2, Appli
37 16 100.0 40 2 US-08-986-948-3 Sequence 3, Appli
38 16 100.0 40 2 US-08-461-216-1 Sequence 1, Appli
39 16 100.0 40 4 PCT-US92-05700-1 Sequence 1, Appli
40 16 100.0 41 1 US-07-819-361-1 Sequence 1, Appli
41 16 100.0 41 1 US-08-302-808-4 Sequence 4, Appli
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44 16 100.0 42 1 US-07-744-767A-2 Sequence 2, Appli
45 16 100.0 42 1

ALIGNMENTS

RESULT 1
US-08-302-808-10
; Sequence 10, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: OKADA, Asano
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Wed Sep 13 08:11:34 2000

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; TOPOLOGY: linear
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; HYPOTHETICAL: NO
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; US-08-302-808-10

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US-08-986-948-10
; Sequence 10, Application US/08986948
; Patent No. 595317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 595317uhiro
; APPLICANT: OKADA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
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; APPLICATION NUMBER: US/08/986,948
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; TOPOLOGY: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-10

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RESULT 3
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; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-08-659-984A-18

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RESULT 4
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US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-11

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder

STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-12

Query Match 100.0%; Score 16; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9 DAEFRHDSGYEVHHQK 24
|||||

RESULT 6
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:

Wed Sep 13 08:11:34 2000

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; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-11

Query Match 100.0%; Score 16; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 7
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; Sequence 12, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8080
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-12

Query Match 100.0%; Score 16; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 8
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4

Query Match 100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9
US-08-302-808-7

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; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-302-808-7

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Query Match      100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

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RESULT 10
US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth

```

```

; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-609-090-2

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Query Match      100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

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RESULT 11
US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, NO. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948

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1

TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: {SYMBOL 98 \f "Symbol"}\A4(1-28);
DESCRIPTION: page 83, line 31
US-08-461-216-2

Query Match 100.0%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14
US-08-609-090-3
Sequence 3, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-3

Query Match 100.0%; Score 16; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

RESULT 15
US-08-609-090-4
Sequence 4, Application US/08609090

Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-4

Query Match 100.0%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

Search completed: September 13, 2000, 02:25:26
Job time: 169 sec

us-09-155-076-2.rai

Wed Sep 13 08:11:34 2000

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+	16.00	351.86	1.7e-11	58	AR016774	Sequence 15 from Patent
+	16.00	349.24	2.3e-11	85	A49528	Sequence 10 from Patent
+	16.00	345.07	4.0e-11	156	A69920	Sequence 15 from Patent
+	16.00	344.28	4.4e-11	175	X56127	S. crofa mRNA for amyloid
+	16.00	344.28	4.4e-11	175	X56128	U. maritimus mRNA for amyloid
+	16.00	344.25	4.5e-11	176	X56125	C. familiaris mRNA for amyloid
+	16.00	344.25	4.5e-11	176	X56129	Oryctolagus sp. mRNA for amyloid
+	16.00	344.21	4.5e-11	177	X56126	Cavia sp. mRNA for amyloid
+	16.00	344.17	4.5e-11	177	X56124	B. taurus sp. mRNA for amyloid
+	16.00	343.76	4.7e-11	178	X56130	Ovis sp. mRNA for amyloid
+	16.00	342.06	5.9e-11	189	M2969	Human amyloid protein gene
+	16.00	342.06	5.9e-11	189	M37895	Human amyloid-beta protein
+	16.00	341.95	6.0e-11	246	S60721	beta-amyloid peptide precursor
+	16.00	341.95	6.0e-11	246	S61380	beta-amyloid peptide precursor
+	16.00	341.95	6.0e-11	246	S61383	beta-amyloid peptide precursor
+	16.00	341.99	6.6e-11	275	I13479	Human PREA4 gene for Alzheimer's
+	16.00	340.59	7.1e-11	300	I06131	Sequence 21 from Patent
+	16.00	340.59	7.1e-11	300	I08767	Sequence 14 from Patent
+	16.00	339.45	8.2e-11	354	A69499	Sequence 2 from Patent
+	16.00	339.45	8.2e-11	354	A69501	Sequence 4 from Patent
+	16.00	339.45	8.2e-11	354	A69503	Sequence 6 from Patent
+	16.00	339.45	8.2e-11	354	A69505	Sequence 8 from Patent
+	16.00	339.45	8.2e-11	354	A69507	Sequence 10 from Patent
+	16.00	339.45	8.2e-11	354	A72176	Sequence 2 from Patent
+	16.00	339.45	8.2e-11	354	A72178	Sequence 4 from Patent
+	16.00	339.45	8.2e-11	354	A72180	Sequence 6 from Patent
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+	16.00	336.39	1.2e-10	553	AR007224	Sequence 9 from Patent
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11 GACGCTGAATTTAGACAGACTCTGGTTACGAAGTTCACCAAAAG 58

seq_name: gb_pat:A69920

seq_documentation_block:
LOCUS A69920 156 bp DNA PAT 07-MAY-1999
DEFINITION Sequence 15 from Patent W09807850.
ACCESSION A69920
VERSION A69920.1 GI:4774427
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 156)
AUTHORS Preddie,E.R. and Bergmann,J.E.
TITLE AGENTS FOR PRE-SYMPTOMATIC DETECTION AND THERAPEUTIC TARGETING OF
ALZHEIMER'S DISEASE AND DOWN SYNDROME IN HUMANS
JOURNAL PATENT: WO 9807850-A 26-FEB-1998;
PREDDIE ENRIQUE R (CA)
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Location/Qualifiers
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Percent Similarity: 100.000 Percent Identity: 100.000

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seq_name: gb_om:SSAPPMR

seq_documentation_block:
LOCUS SSAPPMR 175 bp mRNA MAM 14-JUL-1992
DEFINITION S.scrofa mRNA for amyloid precursor protein.
ACCESSION X56127
VERSION X56127.1 GI:1895
KEYWORDS amyloid polypeptide.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Suidae; Sus.
REFERENCE
1 (bases 1 to 175)
AUTHORS Johnstone,E.M.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE
2 (bases 1 to 175)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES
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seq_documentation_block:
LOCUS UMAPPMR 175 bp mRNA MAM 14-JUL-1992
DEFINITION U.maritimus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56128
VERSION X56128.1 GI:2165
KEYWORDS amyloid polypeptide.
SOURCE polar bear.
ORGANISM Thalarchos maritimus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Fissipedia; Ursidae; Thalarchos.
REFERENCE
1 (bases 1 to 175)
AUTHORS Johnstone,E.M.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE
2 (bases 1 to 175)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES
Location/Qualifiers
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seq_name: gb_om:CFAPPMR

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 DEFINITION C.familiaris mRNA for amyloid precursor protein (APP) (partial).
 ACCESSION X56125
 VERSION X56125.1 GI:872
 KEYWORDS amyloid polypeptide.
 SOURCE dog.

ORGANISM

Canis familiaris
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Carnivora; Fissipedia; Canidae; Canis.

REFERENCE

1 (bases 1 to 176)
 Johnstone, E.M.
 Direct Submission

JOURNAL

Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE

2 (bases 1 to 176)
 Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and
 Little, S.P.

AUTHORS

Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis
 Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
 92017079

FEATURES

Location/Qualifiers

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 /db_xref="taxon:9615"
 /tissue_type="kidney"
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BASE COUNT

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ORIGIN

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 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

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 US-09-155-076-2 x CFAPPMR ..
 Align seg 1/1 to: CFAPPMR from: 1 to: 176

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 19 GATGCCGAGTCCGACATGACTCAGGATGAGTTCATCATCAGAAA 66

seq_name: gb_om:ORAPPMR

seq_documentation_block:
 LOCUS ORAPPMR 176 bp mRNA MAM 14-JUL-1992
 DEFINITION Oryctolagus sp. mRNA for amyloid precursor protein (APP) (partial).
 ACCESSION X56129
 VERSION X56129.1 GI:1817
 KEYWORDS amyloid polypeptide.
 SOURCE Oryctolagus cuniculus.
 ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Lagomorpha; Leporidae; Oryctolagus.

REFERENCE

1 (bases 1 to 176)
 Johnstone, E.M.

AUTHORS

TITLE

Direct Submission

JOURNAL

Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
 LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA

REFERENCE

2 (bases 1 to 176)
 Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and
 Little, S.P.

AUTHORS

TITLE

JOURNAL

MEDLINE

FEATURES

source

CDS

FEATURES

source

CDS

FEATURES

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Wed Sep 13 08:11:34 2000

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REFERENCE
AUTHORS      2 (bases 1 to 176)
              Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
              Little,S.P.
TITLE        Conservation of the sequence of the Alzheimer's disease amyloid
              peptide in dog, polar bear and five other mammals by cross-species
              polymerase chain reaction analysis
JOURNAL      Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE      92017079
FEATURES     Location/Qualifiers
              1..176
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              /db_xref="taxon:10143"
              /tissue_type="brain"
              <1..>176
              /codon_start=1
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              /protein_id="CAA39591.1"
              /db_xref="GI:49570"
              /translation="ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG
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BASE COUNT   52 a 30 c 46 g 48 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x CSAPPMR ..
Align seg 1/1 to: CSAPPMR from: 1 to: 176

1 AspaLaGlupHeArGHisAspSerGlyTyTGluValHisGlnLys 16
|||||
19 GATCGAGAAATCCGACATGACTTCAGGATATGAGATCATCATCAAAA 66
VVIATVIVITLMLK"

seq_name: gb_om:BTAPPMR

seq_documentation_block: 177 bp mRNA MAM 14-JUL-1992
LOCUS BTAPPMR
DEFINITION B.taurus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56124
VERSION X56124.1 GI:82
KEYWORDS amyloid polypeptide.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
92017079
JOURNAL MEDLINE
FEATURES Location/Qualifiers
  1..177
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  /db_xref="taxon:9913"
  /tissue_type="brain"
  <1..>177
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  /product="amyloid precursor protein"
  /protein_id="CAA39591.1"
  /db_xref="GI:83"

CDS

REFERENCE
AUTHORS      2 (bases 1 to 177)
              Johnstone,E.M.
              Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
              LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
TITLE        Conservation of the sequence of the Alzheimer's disease amyloid
              peptide in dog, polar bear and five other mammals by cross-species
              polymerase chain reaction analysis
JOURNAL      Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE      92017079
FEATURES     Location/Qualifiers
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              /db_xref="taxon:9939"
              /tissue_type="heart"
              <1..>178
              /codon_start=3
              /product="amyloid precursor protein"
              /protein_id="CAA39595.1"
              /db_xref="GI:1830"
              /db_xref="SWISS-PROT:Q28757"
              /translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
              VVIATVIVITLMLK"
              VVIATVIVITLMLK"
BASE COUNT   48 a 31 c 49 g 50 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ..
Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspaLaGlupHeArGHisAspSerGlyTyTGluValHisGlnLys 16
|||||
19 GATCGAGAAATCCGACATGACTTCAGGATATGAGATCATCATCAAAA 66
VVIATVIVITLMLK"

seq_name: gb_om:OVAPPMR

seq_documentation_block: 178 bp mRNA MAM 14-JUL-1992
LOCUS OVAPPMR
DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56130
VERSION X56130.1 GI:1829
KEYWORDS amyloid polypeptide.
SOURCE Ovis sp.
ORGANISM Ovis sp.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovidae; Caprinae;
Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and
Little,S.P.
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
92017079
JOURNAL MEDLINE
FEATURES Location/Qualifiers
  1..178
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  /db_xref="taxon:9939"
  /tissue_type="heart"
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  /product="amyloid precursor protein"
  /protein_id="CAA39595.1"
  /db_xref="GI:1830"
  /db_xref="SWISS-PROT:Q28757"
  /translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV
  VVIATVIVITLMLK"
  VVIATVIVITLMLK"
BASE COUNT   48 a 31 c 49 g 50 t
ORIGIN

alignment_scores:
  Quality: 16.00      Length: 16
  Ratio: 1.000       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ..
Align seg 1/1 to: OVAPPMR from: 1 to: 178

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
 |||
 18 GATGCAGAAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 65

seq_name: gb_pr1:HUMAPR4A1

seq_documentation_block:
 LOCUS HUMAPR4A1 189 bp DNA PRI 31-OCT-1994
 DEFINITION Human amyloid protein gene, exon X.
 ACCESSION M29269
 VERSION M29269.1 GI:178862
 KEYWORDS amyloid protein.
 SEGMENT 1 of 2
 ORGANISM Homo sapiens
 Human DNA (library of T. Maniatis), clone lambda-41.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 189)
 AUTHORS Johnstone,E.M., Chaney,M.O., Moore,R.E., Ward,K.E., Norris,F.H. and Little,S.P.
 TITLE Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor
 JOURNAL Biochem. Biophys. Res. Commun. 163 (3), 1248-1255 (1989)
 MEDLINE 89392030
 FEATURES Location/Qualifiers

source

intron

exon

BASE COUNT

ORIGIN

alignment_scores:

Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x HUMAPR4A1 ..

Align seg 1/1 to: HUMAPR4A1 from: 1 to: 189

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
 |||
 93 GATGCAGAAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 140

seq_name: gb_pr1:HUMAMYBBI

seq_documentation_block:
 LOCUS HUMAMYBBI 242 bp DNA PRI 31-OCT-1994
 DEFINITION Human amyloid-beta protein DNA, exon 14.
 ACCESSION M37895
 VERSION M37895.1 GI:178617
 KEYWORDS amyloid-beta protein.
 SEGMENT 1 of 2
 SOURCE Human (Dutch patient with hereditary cerebral hemorrhage with amyloidosis) DNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

Levy,E., Carman,M.D., Fernandez-Madrid,I.J., Power,M.D., Lieberburg,I., van Duinen,S.G., Bots,G.T., Luyendijk,W. and Frangione,B.

TITLE

Mutation of the Alzheimer's disease amyloid gene in hereditary

JOURNAL Science 248 (4959), 1124-1126 (1990)
 MEDLINE 90260663
 FEATURES Location/Qualifiers

source

1. .242
 /organism="Homo sapiens"
 /isolate="hereditary cerebral hemorrhage with amyloidosis of Dutch type patient"
 /db_xref="taxon:9606"
 /map="21q21.2"

intron

exon

intron

BASE COUNT

ORIGIN

alignment_scores:

Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x HUMAMYBBI ..

Align seg 1/1 to: HUMAMYBBI from: 1 to: 242

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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 154 GATGCAGAAATCCGACATGATTCGGATATGAAGTTCATCATCAAAA 201

seq_name: gb_pr2:S60721

seq_documentation_block:

LOCUS S60721 246 bp mRNA PRI 23-JUL-1993
 DEFINITION beta-amyloid peptide precursor (clone 1) [human, mRNA Partial Mutant, 246 nt].

ACCESSION S60721

VERSION S60721.1 GI:299644

KEYWORDS

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor

JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)

MEDLINE 93236601

REMARK

GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 129915] from the original journal article.

This sequence comes from Fig. 1.

Map location: 21.

FEATURES

source

1. .246

/organism="Homo sapiens"

/db_xref="taxon:9606"

1. .246

/partial

/gene="beta-amyloid peptide precursor, beta App"

/partial

/gene="beta-amyloid peptide precursor, beta App"

/note="This sequence comes from Fig. 1; Protein sequence is in conflict with the conceptual translation;

mismatches(44[K->N],73[W->Y],76[I->N]); beta App"

/codon_start=1

/product="beta-amyloid peptide precursor"

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alignment_block:
US-09-155-076-2 x S61380
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Align seg 1/1 to: S61380 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61383

seq_documentation_block:
LOCUS S61383 246 bp mRNA PRI 23-JUL-1993
DEFINITION beta-amyloid peptide precursor [clone 3] [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61383
VERSION S61383.1 GI:299648
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman,R.B., Rosenzwaig,R. and Miller,D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132966] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
Location/Qualifiers
source 1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
CDS 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
/note="this sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(698[K->N],727[W->Y],730[I->N]); beta APP"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26265.1"
/db_xref="GI:299649"
/translation="GSGLTNKTETISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGALLGLMGVGVIAIVIGITLVMLKKQWTSIHGVE"

BASE COUNT 72 a 40 c 71 g 63 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x S60721
..
Align seg 1/1 to: S60721 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61380

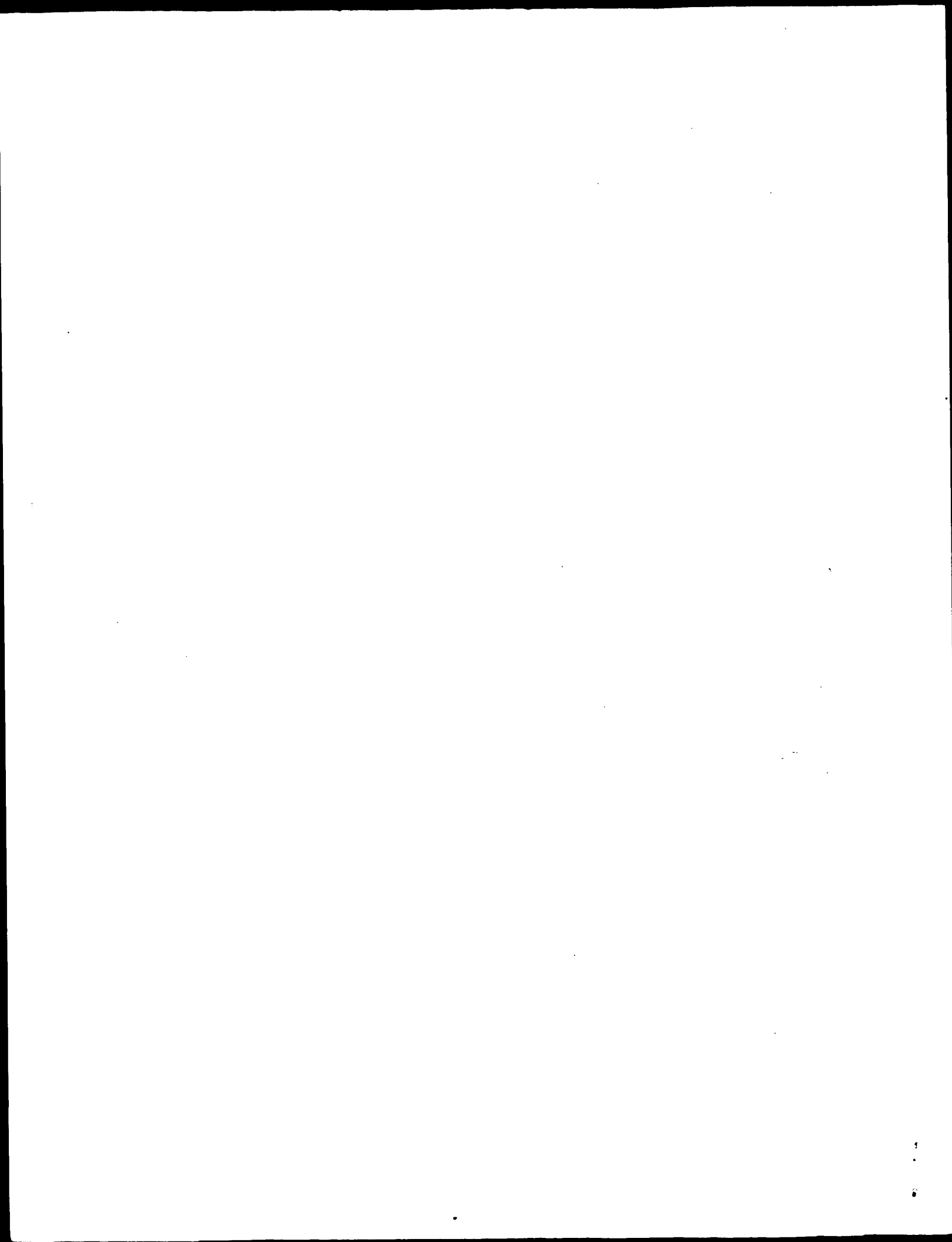
seq_documentation_block:
LOCUS S61380 246 bp mRNA PRI 23-JUL-1993
DEFINITION beta-amyloid peptide precursor [clone 2] [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61380
VERSION S61380.1 GI:299646
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman,R.B., Rosenzwaig,R. and Miller,D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132963] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
Location/Qualifiers
source 1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
CDS 1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
/note="this sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(44[K->N],73[W->Y],76[I->N]); beta APP"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26264.1"
/db_xref="GI:299647"
/translation="GSGLTNKTETISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGALLGLMGVGVIAIVIGITLVMLKKQWTSIHGVE"

BASE COUNT 73 a 40 c 69 g 64 t
ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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OM of: US-09-155-076-2 to: N_Geneseq_36.* out_format : pfs

Date: Sep 13, 2000 3:50 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODE=framet-p2n.model -DEV=xlp
-O/csn2.1/USPTO.spool/US09155076/runat_29082000_092539_16943/app_query.fasta_1.144
-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=ring -GAPOP=4.500
-IGAPEXT=0.050 -MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000
-IGAPOP=4.500 -QGAPEXT=0.050 -GAPOP=60.000 -XGAPEXT=60.000
-DELOP=6.000 -FGAPEXT=7.000 -GAPOP=60.000 -XGAPEXT=60.000
-TRANS=human40.cdi -LST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09155076 -CGN1_1.75 -NCPU=6 -ICPU=3
-LOGLOG -NO_XLPXY -WAIT -THREADS=1
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: N_Geneseq_36.*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.910000

WARN: XGAPOP and XGAPEXT must be equal. Assuming XGAPOP=XGAPEXT=60.000

WARN: XGAPEXT and XGAPEXT must be equal. Assuming XGAPEXT=XGAPEXT=60.000

score_list:

Sequence	Std	Orig	ZScore	EScore	Len	Documentation
N_Geneseq_36:T38687	+	16.00	336.34	3.9e-11	58	Mouse amyloid precursor protein
N_Geneseq_36:T14516	+	16.00	338.80	5.4e-11	85	Beta-amyloid peptide coding sequence
N_Geneseq_36:N92266	+	16.00	328.94	1.0e-10	177	Region of pre-APP coding sequence
N_Geneseq_36:Q77992	+	16.00	328.50	1.1e-10	189	CDNA encoding the APP leader sequence
N_Geneseq_36:V23754	+	16.00	326.34	1.4e-10	262	Alzasi coding sequence. Nucleic
N_Geneseq_36:Q88696	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88697	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88698	+	16.00	325.51	1.6e-10	297	Beta-amyloid precursor protein
N_Geneseq_36:Q10017	+	16.00	325.44	1.6e-10	300	Sequence encoding beta-amyloid
N_Geneseq_36:Q42665	+	16.00	325.44	1.6e-10	300	Full-length beta-amyloid protein
N_Geneseq_36:Q88699	+	16.00	325.24	1.6e-10	309	Beta-amyloid precursor protein
N_Geneseq_36:Q88700	+	16.00	325.24	1.6e-10	309	Beta-amyloid precursor protein
N_Geneseq_36:T18082	+	16.00	324.69	1.7e-10	336	Familial Alzheimer's disease APP
N_Geneseq_36:V20377	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20380	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20381	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20379	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20378	+	16.00	324.34	1.8e-10	354	DNA for APP C-terminal fragment
N_Geneseq_36:V07188	+	16.00	324.34	1.8e-10	354	Flag-amyloid precursor protein
N_Geneseq_36:X08982	+	16.00	324.34	1.8e-10	354	Amyloid precursor protein (APP)
N_Geneseq_36:V20382	+	16.00	324.23	1.9e-10	360	DNA for APP C-terminal fragment
N_Geneseq_36:N80605	+	16.00	322.24	2.4e-10	486	Lambda SM2 encoding first 18 am
N_Geneseq_36:Q10015	+	16.00	322.24	2.4e-10	486	Genomic clone including beta-am
N_Geneseq_36:Q42662	+	16.00	322.24	2.4e-10	486	Clone Lambda SM2 encoding beta-am
N_Geneseq_36:Q82910	+	16.00	321.79	2.5e-10	520	Human beta amyloid fusion prote
N_Geneseq_36:V23753	+	16.00	321.59	2.6e-10	536	Alzasi coding sequence. Nucleic
N_Geneseq_36:N90457	+	16.00	324.75	6.2e-10	1504	CDNA sequence of clone amy 37
N_Geneseq_36:V36436	+	16.00	314.68	6.3e-10	1521	Maltose binding protein-APP (S
N_Geneseq_36:N90397	+	16.00	314.50	6.4e-10	1562	CDNA sequence of amy 37 clone.
N_Geneseq_36:Q54257	+	16.00	313.86	7.0e-10	1721	APP-REP 751 amyloid precursor
N_Geneseq_36:Q69003	+	16.00	312.59	8.2e-10	2085	Mouse amyloid precursor protei
N_Geneseq_36:Q27801	+	16.00	312.58	8.3e-10	2088	APP695. Polynucleotide probe c
N_Geneseq_36:N80604	+	16.00	312.06	8.8e-10	2256	Lambda APCP16814, amino acids
N_Geneseq_36:Q10014	+	16.00	312.06	8.8e-10	2256	Clone lambda APCP16814 of beta
N_Geneseq_36:Q20532	+	16.00	312.06	8.8e-10	2256	Sequence of clone lambdaAPC16
N_Geneseq_36:Q42661	+	16.00	312.06	8.8e-10	2256	Lambda clone APCP16814 encodes
N_Geneseq_36:Q27802	+	16.00	312.04	8.8e-10	2265	APP751. Polynucleotide probe c
N_Geneseq_36:X08983	+	16.00	311.91	9.0e-10	2310	Amyloid precursor protein (APP)
N_Geneseq_36:V10322	+	16.00	311.91	9.0e-10	2310	Human APP770 cDNA. Identifying

N_Geneseq_36:Q48860 + 16.00 311.90 9.0e-10 2313 ! Mutated APP770 exon 17 DNA.
N_Geneseq_36:Q74708 + 16.00 311.90 9.0e-10 2313 ! cDNA of APP 770 gene contg.
N_Geneseq_36:N91050 + 16.00 310.29 1.1e-09 2949 ! Sequence encoding novel amy
N_Geneseq_36:Q05086 + 16.00 310.29 1.1e-09 2949 ! Sequence encodes NAP-2 gene
N_Geneseq_36:N91049 + 16.00 310.16 1.1e-09 3006 ! Sequence encoding novel amy
N_Geneseq_36:Q05085 + 16.00 310.16 1.1e-09 3006 ! Sequence encodes NAP gene a

seq_name: N_Geneseq_36:T38687

seq_documentation_block:

ID T38687 standard; DNA; 58 BP.

AC T38687;

DE 21-JUL-1997 (first entry)

DE Mouse amyloid precursor protein exon 16 primer ST61.

KW Exon 16; murine; mouse; amyloid; precursor; protein; APP;

KW humanisation; homozygous; heterozygous; human; Abeta; Swedish;

KW familial; Alzheimer's; disease; FAD; mutation; tool; model;

KW elucidation; pathology; symptomatology; screen; inhibition;

KW transgenic; polymerase chain reaction; primer; PCR;

KW amplification; ss.

OS Synthetic.

PN W09634097-A1.

PD 31-OCT-1996.

PF 26-APR-1996; U05824.

PR 26-APR-1995; US-429207.

PR 23-APR-1996; US-636876.

PA (CEPH-) CEPHALON INC.

PI Hoffman EK, Reaume AG, Scott RW, Siman R, Trusko SP;

DR WPI; 96-497629/49.

PT Transgenic mice with humanised amyloid precursor protein gene -

PT having at least 1 Swedish FAD mutation, useful as tools or models to

PT elucidate role of human A-beta in Alzheimer's disease

PS Example 1; Page 75; 123pp; English.

CC The present sequence is a primer for the PCR amplification of exon

CC 16 of the mouse amyloid precursor protein (APP) gene, into which 6

CC humanising base pair changes were introduced. The exon was then used

CC in the preparation of mice homozygous or heterozygous for a

CC targeted APP encoding gene, comprising a human Abeta peptide

CC encoding sequence in place of the endogenous murine sequence, and

CC at least 1 Swedish Familial Alzheimer's Disease (FAD) mutation. The

CC mice can be used as tools, or models to elucidate the role of human

CC Abeta in AD pathology and symptomatology. They can also be used to

CC screen chemical compounds for the ability to inhibit in vivo

CC processing of APP, to yield the human Abeta peptide by

CC administering the chemical compounds to a mouse and measuring the

CC relative amounts of amyloidogenic and nonamyloidogenic processing

CC of APP in a sample from the mouse at an appropriate interval after

CC administration of the chemical compounds.

SQ Sequence 58 BP; 23 A; 11 C; 13 T;

alignment_scores:

Quality: 16.00 Length: 16

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x T38687 ..

Align seg 1/1 to: T38687 from: 1 to: 58

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||

8 GATGCAGAAATTCAGACATGATTCAGGATATGAAGTCCACCATCAAAA 55

seq_name: N_Geneseq_36:T14516

seq_documentation_block:

ID T14516 standard; DNA; 85 BP.

AC T14516;

DT 30-OCT-1996 (first entry)

DE Beta-amyloid peptide coding sequence.

UNfolded-protein-response element; UPR; BiP; expression cassette; p53;

reporter element; protein malforming; prion; beta-amyloid peptide; plant; host cell; animal; insect cell; fungal cell; saccharomyces cerevisiae; protein aggregation inhibitor; Alzheimer's disease; cancer; therapy; ds. Synthetic.

Key misc_feature 1. .60 Location/Qualifiers
/tag= a
/note= "5' overhang"
misc_feature complement (85)
/tag= b
/note= "site of 60 bp 5' overhang"

WO9608561-AL.
21-MAR-1996.
04-SEP-1995; E03475.
16-SEP-1994; EP-810536.
(CIBA) CIBA GEIGY AG.
Chaudhuri B, Stephan C;
WPI; 96-179938/18.
Host used to determined influence of cpd. on appearance of malformed protein - also to identify cpds. that inhibit the aggregation of protein, pref. beta-amyloid, useful in treatment of Alzheimer's disease

Example 10: Page 18: 59pp; English.
This sequence represents the beta-amyloid4 peptide. This sequence is amplified using the primers shown in T14517 and T14518, and is used in one of the expression cassettes of the invention. The first expression cassette contains one or more copies of the unfolded-protein-response (UPR) element (see T14511) operably linked to a reporter element. The second expression cassette comprises a promoter operably linked to a signal sequence, a DNA encoding a protein whose malforming is to be studied, and a terminator sequence. The protein encoding sequence in the second expression cassette is preferably a prion, p53, beta-amyloid peptide, or functional derivatives of these. The two cassettes are used to transform a host cell that is capable of excreting proteins. The host cell can be a plant, animal or insect cell, but is preferably a fungal cell (especially saccharomyces cerevisiae). The transformed host can be used to determine the influence of a compound on the appearance of a malformed protein. This is done by culturing the host cell under suitable conditions, applying the compound to be tested and measuring the amount of reporter gene activation. Compounds identified by this method can be used to inhibit protein aggregation, especially for the treatment of Alzheimer's disease or cancer.

Sequence 85 BP; 22 A; 18 C; 21 G; 24 T;

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x T14516 ..

Align seg 1/1 to: T14516 from: 1 to: 85

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
11 GACGCTGAATTTAGACACGACTCTGTTACGAAGTTCACCAACAAAG 58

seq_name: N_Geneseq_36:N92266

seq_documentation_block:
ID N92266 standard; RNA; 177 BP.
AC N92266;
DT 23-APR-1990 (first entry)
DE Region of pre-APC coding sequence.
KW Alzheimer's disease; pre-APC coding sequence; APC protein.
EP-341491-A.
PN 15-NOV-1989.
PF 26-APR-1989; 107531.
PR 13-MAY-1988; US-194053.
PA (MOLE-) Molecular Therapeutics Inc.
PI Scangos G. Rae P, Unterbeck A, Kamarck ME;

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 58 GATCAGATTCCGACATGACTAGGATATGAGATTCATCATCAAAA 105

seq_name: N_Geneseq_36:V23754

seq_documentation_block:

ID V23754 standard; DNA; 262 BP.
 AC V23754;
 DT 18-AUG-1998 (first entry)
 DE AlzAs1 coding sequence.
 KW DSAs; DSASP; alzAs; Down's syndrome; diagnosis; therapy; human;
 KW Alzheimer's disease; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 50..205
 FT /*tag= a
 FT /product= ALZAspl
 FT /note= "specifically claimed fragment"

PN WO9807850-A2.
 PD 26-FEB-1998.
 PF 22-AUG-1997; E04599.
 PR 22-AUG-1996; CA-183901.
 PA (BERG/) BERGMANN J E.
 PA (BERG/) BERGMANN J E.
 PI Bergmann JE, Preddie ER;
 DR WPI; 98-169155/15.
 DR P-PSDB; W53984.
 PT Nucleic acid molecules dsas, and alzAs - used for detecting and
 PT treating Down's syndrome and Alzheimer's disease
 PS Claim 13; Fig 11; 96pp; English.
 CC This sequence represents the human alzAs1 nucleic acid. The dsas
 CC and alzAs DNA sequences are the nucleic acids of the invention. Reagents
 CC specifically for DSASP can be used for the diagnosis of Down's syndrome
 CC in humans and especially in pregnant women. Molecules that inhibit the
 CC activity of the promoters (PDS1, PDS2, PDS3, and PDS4) for dsas can be
 CC used for treating Down's syndrome. The reagent capable of detecting
 CC alzAs can be used for detecting Alzheimer's disease, especially in the
 CC pre-symptomatic stage. Substances that inhibit the promoters for alzAs
 CC can be used in treating Alzheimer's disease.
 SQ Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;

alignment_scores:

Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x V23754 ..

Align seg 1/1 to: V23754 from: 1 to: 262

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 53 GATCAGATTCCGACATGACTAGGATATGAGATTCATCATCAAAA 100

seq_name: N_Geneseq_36:Q88696

seq_documentation_block:

ID Q88696 standard; cDNA to mRNA; 297 BP.
 AC Q88696;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide gene.
 KW Human; beta-amyloid precursor protein; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.

PA (FARH) HOECHST JAPAN KK.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI; 95-180492/24.
 DR P-PSDB; R74694.
 PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types
 PS Claim 2; Page 11; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The DNA may be transferred along with an
 CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells of
 CC a non-human mammal, and the resulting transgenic animal may be used
 CC as a model for Alzheimer disease (AD). The animal model exhibits
 CC symptoms similar to AD, producing large quantities of APP C-terminal
 CC peptide, death of neuron cells in pyramidal cells at cerebral
 CC amyloid regions, increases in glial cells and deposition of
 CC abnormally phosphorylated tau protein. The animal model may be
 CC used to develop new therapies for AD, including gene therapy
 CC strategies.
 SQ Sequence 297 BP; 86 A; 64 C; 78 G; 69 T;

alignment_scores:

Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q88696 ..

Align seg 1/1 to: Q88696 from: 1 to: 297

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 1 GATCAGATTCCGACATGACTAGGATATGAGATTCATCATCAAAA 48

seq_name: N_Geneseq_36:Q88697

seq_documentation_block:

ID Q88697 standard; cDNA to mRNA; 297 BP.
 AC Q88697;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST JAPAN KK.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI; 95-180492/24.
 DR P-PSDB; R74695.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types
 PS Claim 2; Page 12-13; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu
 CC to Gln conversion at codon-22. The DNA may be transferred along
 CC with an APP signal peptide gene (e.g. Q88695) into somatic and germ
 CC cells of a non-human mammal, and the resulting transgenic animal may
 CC be used as a model for Alzheimer disease (AD). The animal model
 CC exhibits symptoms similar to AD, producing large quantities of APP
 CC C-terminal peptide, death of neuron cells in pyramidal cells at
 CC cerebral amyloid regions, increases in glial cells and deposition
 CC of abnormally phosphorylated tau protein. The animal model may
 CC be used to develop new therapies for AD, including gene therapy
 CC strategies.
 SQ Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;

Wed Sep 13 08:11:35 2000

us-09-155-076-2.rng

```

AC 14-MAR-1991 (first entry)
DE Sequence encoding beta-amyloid-related protein.
KW Alzheimer's disease; AD; acute pancreatitis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..300
FT cds /*tag= a
PN WO9014840-A.
PD 13-DEC-1990.
PF 04-JUN-1990; U03141.
PR 06-JUN-1989; US-361912.
PR 29-MAR-1990; US-502273.
PA (CALB-) CALIF BIOTECH INC.
PI Schilling JW, Ponte PA, Cordell B;
DR WPI; 91-006983/01.
DR R-PSDB; R10024.
PT DNA sequences, and protease inhibitors encoded by them and
PT antibodies - for diagnosis and treatment of alzheimers disease
PS Disclosures: Fig 5; 96pp; English.
CC Sequence may be useful in prognosis and diagnosis of human
CC Alzheimer's disease (AD). Abs may be raised to the gene product, and
CC probes derived from the encoding sequence allowing diagnosis and
CC determination of genetic predisposition.
CC The gene product is a protease inhibitor and may also have utility
CC in treatment of acute pancreatitis.
SQ Sequence 300 BP; 87 A; 63 C; 80 G; 70 T;

alignment_scores:
  Quality: 16.00 Length: 16
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x Q10017 ..
Align seg 1/1 to: Q10017 from: 1 to: 300

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
4 GATGCAGAAATCCGACATGACTGAGTATGAAGTTTCATCATCAAAAA 51

seq_name: N_Geneseq_36:Q42665
seq_documentation_block:
ID Q42665 standard; cDNA; 300 BP.
AC Q42665.
DE Full-length beta-amyloid protein coding region.
KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..300
FT cds /*tag= a
FT /product= beta-amyloid_protein
FT /note= "full-length coding sequence obtained by
FT combining overlapping clones SM2W3 and
FT SM2W4 (Q42664 and Q42663, respectively)"
FT misc_difference 160..162
FT /*tag= b
FT /codon= seq: AAC; aa: Lys
FT /note= "this codon is AAG in Q42664"
PN US5220013-A.
PD 15-JUN-1993.
PF 17-NOV-1986; 932193.
PR 17-NOV-1986; US-932193.
PR 31-DEC-1986; US-948376.
PR 30-JAN-1987; US-008810.
PR 18-AUG-1987; US-087002.
PR 30-NOV-1989; US-444118.
PA (SCIO-) SCIOS NOVA INC.

alignment_scores:
  Quality: 16.00 Length: 16
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x Q88698 ..
Align seg 1/1 to: Q88698 from: 1 to: 297

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
1 GATGCAGAAATCCGACATGACTGAGTATGAAGTTTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q88698
seq_documentation_block:
ID Q88698 standard; cDNA to mRNA; 297 BP.
AC Q88698.
DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
KW gene transfer; transgenic animal; Alzheimer disease model;
KW gene therapy; ss.
OS Homo sapiens.
PN EP-653154-A.
PD 17-MAY-1995.
PF 07-NOV-1994; 117512.
PR 12-NOV-1993; JP-306026.
PA (FARH) HOECHST JAPAN LTD.
PA (FARH) HOECHST JAPAN KK.
PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
DR WPI; 95-180492/24.
DR P-PSDB; R74696.
PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
PT part of beta-amyloid precursor protein in a gene construct designed for
PT over-expression in various cell types
PS Claim 2: Page 13-14; 32pp; English.
CC The sequence encodes a human brain beta-amyloid precursor protein
CC (APP) mutant C-terminal peptide, and differs from Q88696 by
CC conversion of Val to Ile at codon-46. The DNA may be transferred
CC along with an APP signal peptide gene (e.g. Q88695) into somatic and
CC germ cells of a non-human mammal, and the resulting transgenic animal
CC may be used as a model for Alzheimer disease (AD). The animal model
CC exhibits symptoms similar to AD, producing large quantities of APP
CC C-terminal peptide, death of neuron cells in pyramidal cells at
CC cerebral amyloid regions, increases in glial cells and deposition
CC of abnormally phosphorylated tau protein. The animal model may
CC be used to develop new therapies for AD, including gene therapy
CC strategies.
SQ Sequence 297 BP; 87 A; 64 C; 77 G; 69 T;

alignment_scores:
  Quality: 16.00 Length: 16
  Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x Q88698 ..
Align seg 1/1 to: Q88698 from: 1 to: 297

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
1 GATGCAGAAATCCGACATGACTGAGTATGAAGTTTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q10017
seq_documentation_block:
ID Q10017 standard; DNA; 300 BP.

```

PI Cordell B, Ponte PA;
 DR WPI: 93-205383/25.
 DR P-PSDB; R37866.
 PT DNA sequence useful for detection of Alzheimer's disease - for
 encoding beta amyloid core protein
 PS Disclosure; Fig 5; 40pp; English.
 CC A clone was obtained from the genomic library described in Lawn et al.,
 CC Cell, 15:1157-1174 (1978) which included a 57 base pair segment which
 CC encodes amino acids 1-18 of the beta-amyloid protein, immediately
 CC preceded by a Methionine. A HindIII/KsaI fragment derived from the
 CC genomic clone and containing the 57bp segment was used to isolate cDNA
 CC fragments from a library prepared from temporal and parietal cortical
 CC tissue from a normal human brain. Lambda clone SM2W3 (Q42664) contains
 CC a 5' region segment which has a 6bp overlap with the 3' end of clone
 CC SM2W4 (Q42663). The full-length beta-amyloid protein coding sequence
 CC (Q42665), including an initiator Met residue which is probably
 CC processed in vivo, was obtained by combining the sequences of the
 CC two overlapping clones.
 SQ Sequence 300 BP; 87 A; 65 C; 78 G; 70 T;

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q42665 ..

Align seg 1/1 to: Q42665 from: 1 to: 300

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 4 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 51

seq_name: N_Geneseq_36:Q88699

seq_documentation_block:

ID Q88699 standard; cDNA to mRNA; 309 BP.

AC Q88699;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide gene.
 KW Human; beta-amyloid precursor protein; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST JAPAN KK.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI: 95-180492/24.
 DR P-PSDB; R74697.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 part of beta-amyloid precursor protein in a gene construct designed for
 over-expression in various cell types
 PS Claim 2; Page 15; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The DNA may be transferred along with an
 CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells
 CC of a non-human mammal, and the resulting transgenic animal may be
 CC used as a model for Alzheimer disease (AD). The animal model
 CC exhibits symptoms similar to AD, producing large quantities of APP
 CC C-terminal peptide, death of neuron cells in pyramidal cells at
 CC cerebral amyloid regions, increases in glial cells and deposition
 CC of abnormally phosphorylated tau protein. The animal model may
 CC be used to develop new therapies for AD, including gene therapy
 CC strategies. 309 BP; 91 A; 64 C; 83 G; 71 T;

Sequence 309 BP; 91 A; 64 C; 83 G; 71 T;

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-155-076-2 x Q88699 ..
 Align seg 1/1 to: Q88699 from: 1 to: 309

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq_name: N_Geneseq_36:Q88700

seq_documentation_block:

ID Q88700 standard; cDNA to mRNA; 309 BP.

AC Q88700;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST JAPAN KK.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI: 95-180492/24.
 DR P-PSDB; R74698.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 part of beta-amyloid precursor protein in a gene construct designed for
 over-expression in various cell types
 PS Claim 2; Page 16-17; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) mutant C-terminal peptide, and differs from Q88699 by
 CC conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The
 CC DNA may be transferred along with an APP signal peptide gene (e.g.
 CC Q88695) into somatic and germ cells of a non-human mammal, and the
 CC resulting transgenic animal may be used as a model for Alzheimer
 CC disease (AD). The animal model exhibits symptoms similar to AD,
 CC producing large quantities of APP C-terminal peptide, death of
 CC neuron cells in pyramidal cells at cerebral amyloid regions,
 CC increases in glial cells and deposition of abnormally
 CC phosphorylated tau protein. The animal model may be used to develop
 CC new therapies for AD, including gene therapy strategies.
 SQ Sequence 309 BP; 90 A; 65 C; 82 G; 72 T;

alignment_scores:

Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q88700 ..

Align seg 1/1 to: Q88700 from: 1 to: 309

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 |||||
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq_name: N_Geneseq_36:T18082

seq_documentation_block:

ID T18082 standard; DNA; 336 BP.

AC T18082;
 DT 10-OCT-1996 (first entry)

2
3
4
5

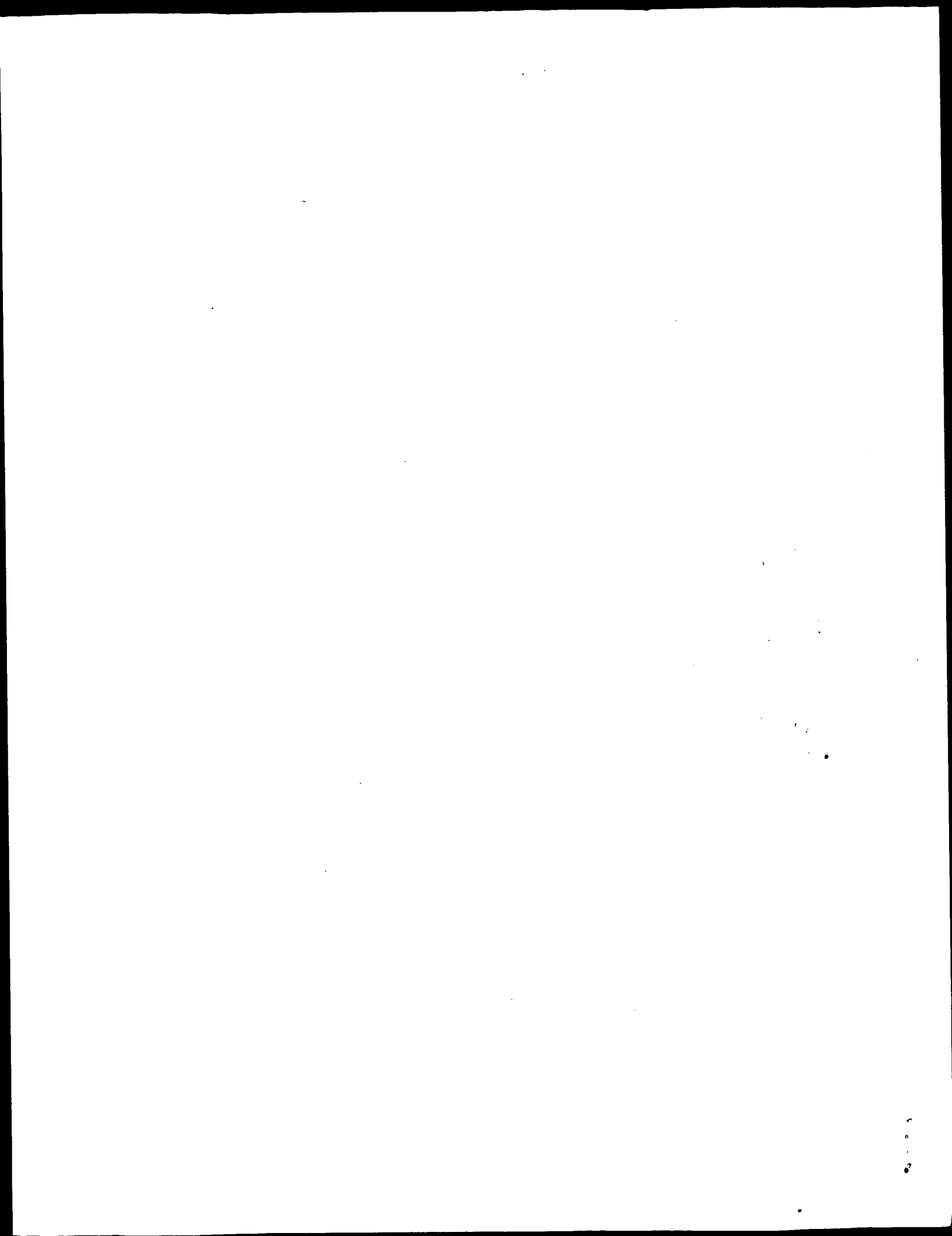
PT or transformed cells, used for identifying potential drugs for
PS Alzheimer's disease
CC Claim 10; Page 11; 15pp; English.
CC The present sequence encodes the human amyloid precursor protein
CC (APP) C-terminal fragment (A4CT) mutant SPA4CT Thr43Ala/Val46Phe.
CC The mutation results in a higher ratio of beta A4 1-42 to beta A4
CC 1-40, useful in disease models to identify potential drugs for the
CC treatment of Alzheimer's disease.
SQ Sequence 354 BP; 91 A; 82 C; 98 G; 83 T;

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x V20380 ..

Align seg 1/1 to: V20380 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
58 GATCCAGAAATCCGACATGACTCAGGATATGAAATTTCATCAAAA 105



;; TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower - 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/04026
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, Ph.D, David W.
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 31188
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; PCT-US94-04026-8

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x PCT-US94-04026-8 ..

Align seg 1/1 to: PCT-US94-04026-8 from: 1 to: 189

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
58 GATGCAGATTCCGACATGCTCAGGATATGAAGTTTCATCATCAAAA 105

seq_name: /cgn2_6/ptodata/2/1na/6_COMB.seq:US-08-339-708A-3

seq_documentation_block:
; Sequence 3, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/339,708A
;; FILING DATE: 14-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 306026/93
;; FILING DATE: 12-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDERCOCK, COLIN G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 026083/0159
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 297 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: homo sapiens
;; STRAIN: human brain
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..297
;; OTHER INFORMATION: /note= "1. human beta-amyloid
;; OTHER INFORMATION: precursor; 2. C-terminal peptide"
;; US-08-339-708A-3

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-339-708A-3 ..

Align seg 1/1 to: US-08-339-708A-3 from: 1 to: 297

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
1 GATGCAGATTCCGACATGCTCAGGATATGAAGTTTCATCATCAAAA 48

seq_name: /cgn2_6/ptodata/2/1na/6_COMB.seq:US-08-339-708A-5

seq_documentation_block:
; Sequence 5, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-5

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; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

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; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
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; STRANDEDNESS: single
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; HYPOTHETICAL: NO
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; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-7

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; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193

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us-09-155-076-2.rni

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; FILING DATE: 17-NOV-1986
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; LENGTH: 300
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; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
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; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kavarabayashi, Takeshi

; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
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; OTHER INFORMATION: precursor; 2. C-terminal peptide"
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seq_documentation_block:
; Sequence 11, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
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; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
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; LENGTH: 309 base pairs
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
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; US-08-339-708A-11

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; Sequence 2, Application US/08729345
; Patent No. 5849999
; GENERAL INFORMATION:
; APPLICANT: Neve, Rachael L. Joanne
; APPLICANT: Berger-Sweeney, Joanne
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL

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; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,345
; FILING DATE: 16-OCT-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/027001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002

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Wed Sep 13 08:11:35 2000

us-09-155-076-2.rni

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;
; FILING DATE: 18-AUG-1987
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; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
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; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
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; NUMBER OF SEQUENCES: 30
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; FILING DATE: 30-NOV-1989
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; APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
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; APPLICATION NUMBER: US/07/361,912
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; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
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seq_documentation_block:
; Sequence 9, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobelli, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; POLYPEPTIDES AND PROTEINS, AND FUSION PROTEINS FOR USE IN
; THE PRODUCTION OF POLYPEPTIDES AND PROTEINS
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; LOCATION: 115..516
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US-08-268-348A-9

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; Sequence 3, Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/08/480,498
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 015270-002200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
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US-08-480-498-3

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us-09-155-076-2.rni

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GenCore version 4.5
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OM protein - protein search, using sw model

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3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	42	PN0512	beta-amyloid prote
2	16	100.0	57	E60045	Alzheimer's diseas
3	16	100.0	57	F60045	Alzheimer's diseas
4	16	100.0	57	G60045	Alzheimer's diseas
5	16	100.0	57	D60045	Alzheimer's diseas
6	16	100.0	57	A60045	Alzheimer's diseas
7	16	100.0	57	B60045	Alzheimer's diseas
8	16	100.0	82	PQ0438	Alzheimer's diseas
9	16	100.0	695	A49795	Alzheimer's diseas
10	16	100.0	770	QR0044	Alzheimer's diseas
11	7	43.8	747	JH0773	Alzheimer's diseas
12	6	37.5	122	S54715	probable aspartate
13	6	37.5	284	J04723	genome polyprotein
14	6	37.5	313	JT0960	polyprotein - pota
15	6	37.5	327	S11435	genome polyprotein
16	6	37.5	330	A26205	coat protein precu
17	6	37.5	379	S13556	genome polyprotein
18	6	37.5	380	G69277	aspartate-chain am
19	6	37.5	397	T11786	genome polyprotein
20	6	37.5	427	JA0073	genome polyprotein
21	6	37.5	453	C69543	hypothetical prote
22	6	37.5	519	PC1072	nuclear inclusion
23	6	37.5	761	T15776	hypothetical prote
24	6	37.5	846	A60678	genome polyprotein
25	6	37.5	1555	JT0959	polyprotein - pota
26	6	37.5	3051	1JN0545	genome polyprotein
27	6	37.5	3063	2JS0166	genome polyprotein
28	5	31.2	58	D69449	hypothetical prote
29	5	31.2	112	B72019	periplasmic divale

```

30      5 31.2 112 2 F81520      periplasmic divale
31      5 31.2 123 2 H72479      probable translati
32      5 31.2 125 2 S68170      ig heavy chain v r
33      5 31.2 132 2 JQ0737      RnpA protein - Mic
34      5 31.2 135 1 R3TW12      ribosomal protein
35      5 31.2 135 2 A34653      cell adhesion prot
36      5 31.2 141 2 H72693      hypothetical prote
37      5 31.2 144 2 S23658      superoxide dismuta
38      5 31.2 145 2 S62510      hypothetical prote
39      5 31.2 161 2 S30698      cyax protein - Esc
40      5 31.2 167 2 T34963      hypothetical prote
41      5 31.2 178 2 T19064      hypothetical prote
42      5 31.2 186 2 T31347      hypothetical prote
43      5 31.2 195 2 B70577      hypothetical prote
44      5 31.2 196 2 S72861      hypothetical prote
45      5 31.2 203 1 BVECRV      ruvA protein - Esc

```

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 16; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 4.2e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp (sheep)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 5.5e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 6 DAEFRHDSGYEVHHQK 21

```
RESULT 3
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21
```

```
Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 16; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 5.5e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180
```

A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 16; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 7.6e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 17 DAEFRHDSGYEVHHQK 32

RESULT 9
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 16; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 597 DAEFRHDSGYEVHHQK 612

RESULT 10
 QRHUA
 Alzheimer's disease amyloid beta protein precursor - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor xia inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 24-Nov-1999
 C:Accession: S02260; S05194; A32277; A33260; A33486; I39451; I39453; I59562; A44
 468; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:8128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEMI>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360
 A:Note: alternative splice form APP(695)
 R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:q341202; PIDN:AAC13654.1; PID:q516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AAB59502.1; PID:q178616
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMEVPAFWAEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AAB59501.1; PID:q178615
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Accession: A59020
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AAB19991.1; PID:q236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbom, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Mart
 A. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

Query Match 43.8%; Score 7; DB 2; Length 747;
Best Local Similarity 100.0%;
Pred. No. 1.2;
7. Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 10 YEVHHQ 16
 |||||
 Db 658 YEVHHQ 664

RESULT 12

S54715
 C: probable aspartate transaminase (EC 2.6.1.1) - Streptomyces coelicolor (fragment)
 C: Species: Streptomyces coelicolor
 C: Date: 23-Aug-1995 #sequence_revision 12-Dec-1997 #text_change 13-Sep-1998
 C: Accession: S54715
 R: Puttkhant, C.; Nihira, T.; Yamada, Y.
 Mol. Gen. Genet. 247, 118-122, 1995
 A: Title: Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene of
 A: Reference number: S54715; MUID: 95221511
 A: Accession: S54715
 A: Molecule type: DNA
 A: Residues: 1-122 <PUT>
 A: Cross-references: EMBL:D32254
 A: Experimental source: strain A3(2), substrain SC
 C: Superfamily: aspartate transaminase
 C: Keywords: aminotransferase

Query Match 37.5%; Score 6; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
 |||||
 Db 93 DSGYEV 98

RESULT 13

S04723
 genome polyprotein - potato virus Y (strain o) (fragment)
 N: Contains: coat protein; replicase
 C: Species: potato virus Y, PVY
 C: Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
 C: Accession: S04723
 R: Bravo-Almonacid, F.; Mentaberry, A.N.
 Nucleic Acids Res. 17, 4401, 1989
 A: Title: Nucleotide cDNA sequence coding for the PVY coat protein.
 A: Reference number: S04723; MUID: 89296509
 A: Accession: S04723
 A: Status: translation not shown
 A: Molecule type: genomic RNA
 A: Residues: 1-284 <BRA>
 A: Cross-references: EMBL:X14136; NID: 961445; PIDN: CAA32356.1; PID: 961446
 C: Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology
 C: Keywords: polyprotein

Query Match 37.5%; Score 6; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 6.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
 |||||
 Db 12 YEVHHQ 17

RESULT 14

JT0960
 polyprotein - potato virus Y
 N: Contains: coat protein
 C: Species: potato virus Y, PVY
 C: Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 29-May-1998
 C: Accession: JT0960
 R: Hidaka, M.
 submitted to JIPID, November 1991
 A: Reference number: JT0959

A: Accession: JT0960
 A: Molecule type: genomic RNA
 A: Residues: 1-313 <HID>
 A: Experimental source: necrotic strain T
 C: Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology
 C: Keywords: polyprotein
 F: 46-313/Product: coat protein #status predicted <COA>

Query Match 37.5%; Score 6; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
 |||||
 Db 41 YEVHHQ 46

RESULT 15

S11435
 genome polyprotein - potato virus Y (fragment)
 N: Contains: coat protein; NIB protein
 C: Species: potato virus Y, PVY
 C: Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 20-Sep-1999
 C: Accession: S11435; JCI526
 R: Zhou, X.R.; Fang, R.X.; Wang, C.Q.; Mang, K.Q.
 Nucleic Acids Res. 18, 5554, 1990
 A: Title: cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate).
 A: Reference number: S11435; MUID: 91016851
 A: Accession: S11435
 A: Molecule type: mRNA
 A: Residues: 1-327 <ZHO1>
 A: Cross-references: EMBL:X54058
 R: Zhou, X.R.
 submitted to the EMBL Data Library, July 1990
 A: Reference number: S11549
 A: Accession: S11549
 A: Molecule type: mRNA
 A: Residues: 1-90, 'E', 92-327 <ZHO2>
 A: Cross-references: EMBL:X54038; NID: 961219; PIDN: CAA37993.1; PID: 98333159
 R: Onshima, K.; Hataya, T.; Sano, T.; Inoue, A.K.; Shikata, E.
 Ann. Phytopathol. Soc. Jpn. 57, 615-622, 1991
 A: Title: Comparison of biological properties, serological characteristics and amino a

A: Reference number: JCI526
 A: Accession: JCI526
 A: Molecule type: genomic RNA
 A: Residues: 61-88, 'E', 71-73, 'ES', 76-111, 'S', 113-201, 'E', 203-327 <OHS>
 C: Genetics:

A: Start codon: GCA
 C: Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology
 C: Keywords: coat protein; polyprotein
 F: 61-327/Product: coat protein #status predicted <COP>

Query Match 37.5%; Score 6; DB 2; Length 327;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
 |||||
 Db 55 YEVHHQ 60

Search completed: September 13, 2000, 02:25:56
 Job time: 139 sec

Wed Sep 13 08:11:36 2000

us-09-155-076-2.rpr

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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:27:53 : Search time 10.69 seconds
(without alignments)
46.382 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 16
Sequence: 1 DAEFRHDSGYEVHHOK 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 85661 seqs, 30989116 residues
Word size : 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	57	1	A4_PIG
2	16	100.0	57	1	A4_URDMA
3	16	100.0	58	1	A4_CANFA
4	16	100.0	58	1	A4_RABIT
5	16	100.0	58	1	A4_SHEEP
6	16	100.0	59	1	A4_BOVIN
7	16	100.0	751	1	A4_SAISC
8	16	100.0	770	1	A4_HUMAN
9	6	37.5	213	1	AAT_STRGR
10	6	37.5	284	1	POLG_PVYIO
11	6	37.5	327	1	POLG_PVYCH
12	6	37.5	330	1	COAT_PENV
13	6	37.5	397	1	AAT_STRVG
14	6	37.5	3061	1	POLG_PVYHU
15	6	37.5	3063	1	POLG_PVYN
16	5	31.2	90	1	EFIB_AERPE
17	5	31.2	132	1	RNPA_MICLU
18	5	31.2	135	1	RS12_THETH
19	5	31.2	144	1	SODM_BRAFL
20	5	31.2	145	1	YAF4_SCHPO
21	5	31.2	150	1	RNK6_MIOTA
22	5	31.2	161	1	YZCX_ECOLI
23	5	31.2	203	1	RUVA_ECOLI
24	5	31.2	214	1	ACUB_BACSU
25	5	31.2	218	1	COAT_SMWLM
26	5	31.2	235	1	YVCF_BACSU
27	5	31.2	237	1	CD63_HUMAN
28	5	31.2	237	1	CD63_MOUSE
29	5	31.2	237	1	CD63_RABIT
30	5	31.2	237	1	CD63_RAT
31	5	31.2	258	1	FABI_SVNY3
32	5	31.2	285	1	PNMT_RAT
33	5	31.2	294	1	ATHE_MOUSE

34 5 31.2 303 1 COPB_HUMAN P53618 homo sapien
35 5 31.2 317 1 MAD3_HUMAN P25963 homo sapien
36 5 31.2 329 1 TECB_CHICK P54097 gallus gall
37 5 31.2 331 1 GALR_LACCA O84905 lactobacill
38 5 31.2 331 1 UL38_HCMVA P16779 human cytom
39 5 31.2 336 1 Y724_METH O26820 methanobact
40 5 31.2 340 1 ASTC_PSEAE P80358 pseudomonas
41 5 31.2 369 1 T1B_PARTE Q27180 paramecium
42 5 31.2 372 1 GM4D_VIBCH Q56598 vibrio chol
43 5 31.2 373 1 GM4D_EGOLI P32054 escherichia
44 5 31.2 382 1 MTLD_BACST Q45421 bacillus st
45 5 31.2 398 1 TAP_DROME O16867 drosophila

ALIGNMENTS

RESULT 1
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56127; CAA39592.1; -;
CC HSP; P05067; IAML.
CC DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC DR PROSITE; PS00320; A4_INTRA; PARTIAL.
CC KW Glycoprotein; Amyloid; Neurone; Transmembrane.
CC FT NON_TER 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC FT NON_TER 57
CC SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;

Query Match 100.0%; Score 16; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOK 16

Db 6 DAEFRHDSGYEVHHOK 21

```

[1]
RN SEQUENCE FROM N.A.
RP TISSUE-KIDNEY;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
PROTEIN (BETA-APP)] (FRAGMENT).
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC
CC EMBL; X56125; CAA39590.1; -.
DR HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
FT SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
SQ
Query Match 100.0%; Score 16; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 9.9e-12; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 7 DAEFRHDSGYEVHHQK 22
|||||
RESULT 4
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
PROTEIN (BETA-APP)] (FRAGMENT).
DE DE
DE DE
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
PROTEIN (BETA-APP)] (FRAGMENT).
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; X56128; CAA39593.1; -.
DR HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
SQ
Query Match 100.0%; Score 16; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 9.7e-12; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 6 DAEFRHDSGYEVHHQK 21
|||||
RESULT 3
ID A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
PROTEIN (BETA-APP)] (FRAGMENT).
DE DE
DE DE
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.

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 CC -----

DR EMBL; X56129; CAA39594.1; -;
 DR HSSP; P05067; 1AML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 5
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
 DE PROTEIN (BETA-APP)] (FRAGMENT).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC -----

DR EMBL; X56130; CAA39595.1; -;
 DR HSSP; P05067; 1AML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 9.9e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 6
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
 DE PROTEIN (BETA-APP)] (FRAGMENT).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RA "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----

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 CC -----

DR EMBL; X56124; CAA39589.1; -;
 DR EMBL; X56126; CAA39591.1; -;
 DR HSSP; P05067; 1AML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 58 POTENTIAL.
 FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 59 59
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 16; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Sep 13 08:11:37 2000

us-09-155-076-2.isp

QY 1 DAEFRHDSGYEVHHQK 16
 Db 7 DAEFRHDSGYEVHHQK 22

RESULT 7
 ID A4_SAISC STANDARD; PRT; 751 AA.
 AC Q95241; 1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYL
 DE AMYLOID PROTEIN (BETA-APP)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER, AND KIDNEY;
 RX MEDLINE; 96108492.
 RA Levy E., Anonim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy".
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 CC
 CC EMBL; S81024; AAD14347.1;
 CC PFAM; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA.
 CC PRINTS; PR00204; BETAAMYLOID.
 CC PRINTS; PR00759; BASICPTASE.
 CC PROSITE; PS00280; BPTI_KUNITZ; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC Glycoprotein; Amyloid; Neutone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT CARBOHYD 523 523 PROBABLE.
 FT CARBOHYD 552 552 PROBABLE.
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 SQ SEQUENCE 751 AA; 84893 MB; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 16; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 8.2e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 653 DAEFRHDSGYEVHHQK 668

RESULT 8
 ID A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)
 DE (PN-II) (APPI) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)].
 GN APP OR A4 OR CVAP OR ADL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 87144572.
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
 RA Grzeschik K.H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
 RT cell-surface receptor".
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88122639.
 RA Ponte P., Gonzalez-Bewhitt P., Schilling J., Miller J., Hsu D.,
 RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
 RA Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine
 RT proteinase inhibitors".
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89128427.
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
 RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The PrA4(695) precursor protein of Alzheimer's disease A4 amyloid
 RT is encoded by 16 exons".
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97263807.
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus".
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE; 88122640.
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease".
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE; 88122641.
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity".
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE; 87231971.
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides".
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).

RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE: 88124954.
 RA Zain S.B., Selim M., Chou W.G., Saydel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE: 88035004.
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels."
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE: 90236318.
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene."
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE: 89016647.
 RA Schon E.A., Mica S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide."
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE: 87250462.
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts."
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE: 89384866.
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II."
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE: 90211252.
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor."
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE: 93188965.
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O)."
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE: 92215582.
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein."
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]

RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE: 91104913.
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor."
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE: 92031488.
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein."
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE: 94281210.
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide."
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE: 97128622.
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment."
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE: 98359783.
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RT environment. Is the membrane-spanning domain where we think it is?"
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT Submitted (JUN-1998) to the PDB data bank.
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE: 88296437.
 RA Dyvks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease."
 RL EMBO J. 7:949-957(1988).
 RN [24]
 RP REVIEW.
 RX MEDLINE: 92271194.
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective."
 RL Science 256:780-783(1992).
 RN [25]
 RP REVIEW ON VARIANTS.
 RX MEDLINE: 93250996.
 RA Hardy J.;
 RT "Framing beta-amyloid."
 RL Nat. Genet. 1:233-234(1992).
 RN [26]

Query Match 100.0%; Score 16; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHQQ 16
 Db - 672 DAEFRHDSGYEVHQQ 687

RESULT 9

AAT_STRGR
 ID AAT_STRGR STANDARD; PRT; 213 AA.

P36692;
 AC 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE PROBABLE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A)
 DE (ASPART) (FRAGMENT).
 GN ASPC OR AATA.
 OS Streptomyces griseus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RC MEDLINE; 94314177.
 RA Kuberski S., Kasberg T., Distler J.;
 RT "The nusG gene of Streptomyces griseus: cloning of the gene and
 analysis of the A-factor binding properties of the gene product.";
 RL FEMS Microbiol. Lett. 119:33-39(1994).
 [2]
 RN SEQUENCE OF 1-64 FROM N.A.
 RP STRAIN=IFO 13350;
 RC MEDLINE; 94114580.
 RA Miyake K., Onaka H., Horinouchi S., Beppu T.;
 RT "Organization and nucleotide sequence of the secE-nusG region of
 Streptomyces griseus.";
 RL Biochim. Biophys. Acta 1217:97-100(1994).
 CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE -> OXALOACETATE +
 L-GLUTAMATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 AMINOTRANSFERASES.

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 CC EMBL; X72787; CAA51294.1; -;
 CC EMBL; D17464; -; NOT_ANNOTATED_CDS.
 CC FIR; S41059; S41059.
 CC PROSITE; PS00105; AA_TRANSFR_CLASS_1; PARTIAL.
 KW Transferase; Aminotransferase; Pyridoxal phosphate.
 FT NON_TER 213 213
 SQ SEQUENCE 213 AA; 22693 MW; C380BF59DA55A429 CRC64;
 Query Match 37.5%; Score 6; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 DSGVEV 12
 Db 92 DSGVEV 97
 RESULT 10
 POLG_PVYVO STANDARD; PRT; 284 AA.
 ID POLG_PVYVO
 AC P11897;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)
 (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)].
 DE (FRAGMENT).
 OS Potato virus Y (strain Yo) (PVY).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 89296509.
 RA Bravo-Almonacid F.F., Mentaberry A.N.;
 RT "Nucleotide cDNA sequence coding for the PVYO coat protein.";
 RL Nucleic Acids Res. 17:4401-4401(1989).
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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 CC EMBL; X14136; CAA32356.1; -;
 CC FIR; S04723; S04723.
 CC PFAM; PF00767; Pocy_coat; 1.
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
 FT NON_TER 1 1
 FT CHAIN <1 17 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 18 284 COAT PROTEIN.
 SQ SEQUENCE 284 AA; 31971 MW; E98535C4607898E2 CRC64;
 Query Match 37.5%; Score 6; DB 1; Length 284;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 YEYVHQ 15
 Db 12 YEYVHQ 17
 RESULT 11
 POLG_PVYCH STANDARD; PRT; 327 AA.
 ID POLG_PVYCH
 AC P21294;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB)
 (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)].
 DE (FRAGMENT).
 OS Potato virus Y (strain Chinese isolate) (PVY).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91016851.
 RA Zhou X.R., Fang R.X., Wang C.Q., Mang K.Q.;
 RT "cDNA sequence of the 3'-coding region of PVY genome (the Chinese
 isolate).";
 RL Nucleic Acids Res. 18:5554-5554(1990).
 CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 INDIVIDUAL PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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 CC EMBL; X54058; CAA37993.1; -;

DR PIR; S11549; S11549.
 DR HSP; P05067; 1AMB.
 DR PFAM; PF00767; Poty_coat; 1.
 KW Transferase; RNA-directed RNA polymerase; Coat protein; Polypotein.
 FT NON_TER 1
 FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 61 327 COAT PROTEIN.
 SQ SEQUENCE 327 AA; 36868 MW; 8F8355E2DB6F2F18 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYHHQ 15
 |||||
 Db 55 YEYHHQ 60

RESULT 12
 COAT_PEW
 ID COAT_PEW STANDARD; PRT; 330 AA.
 AC P07993;

DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE COAT PROTEIN.

OS Pepper mottle virus (PeMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.

[1]
 SEQUENCE FROM N.A.
 DR Dougherty W.G., Allison R.F., Parks T.D., Johnston R.E., Feild M.J.,
 RA Armstrong F.B.;
 RT "Nucleotide sequence at the 3' terminus of pepper mottle virus
 RT genomic RNA: evidence for an alternative mode of potyvirus capsid
 RT protein gene organization.";
 RL Virology 146:282-291(1985).

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CC EMBL; M11598; AA46902.1; -
 DR PIR; A26205; A26205.
 DR PFAM; PF00767; Poty_coat; 1.
 KW Coat protein.
 SQ SEQUENCE 330 AA; 37028 MW; C63A2F810D95820E CRC64;

Query Match 37.5%; Score 6; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYHHQ 15
 |||||
 Db 58 YEYHHQ 63

RESULT 13
 AAT_STRVG
 ID AAT_STRVG STANDARD; PRT; 397 AA.
 AC Q60013;

DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A) (ASPAR).

GN ASPC OR AAT.
 OS Streptomyces virginiae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 96257210.
 RA Katayama M., Sakai Y., Okamoto S., Ihara F., Nihira T., Yamada Y.;
 RT "Gene organization in the ada-rplL region of Streptomyces virginiae.";
 RL Gene 171:135-136(1996).
 CC -1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
 CC L-GLUTAMATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.

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CC EMBL; D50624; BAA09299.1; -
 DR PFAM; PF00155; aminotran_1; 1.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS.1; 1.
 KW Transferase; Aminotransferase; Pyridoxal phosphate.
 FT BINDING 236 236 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 397 AA; 42381 MW; EEFEDCEB7D923065 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 397;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
 |||||
 Db 82 DSGYEV 87

RESULT 14
 POLG_PVYHU

ID POLG_PVYHU STANDARD; PRT; 3061 AA.
 AC Q02963;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
 DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
 DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
 DE COAT PROTEIN (CP)).
 DE Potato virus Y (strain Hungarian) (PVY).

OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Viruses;
 OC Potyvirus.

[1]
 SEQUENCE FROM N.A.
 RX MEDLINE; 93154578.

RA Thole V., Dalmay T., Burgan J., Balazs E.;
 RT "Cloning and sequencing of potato virus Y (Hungarian isolate) genomic
 RT RNA.";
 RL Gene 123:149-156(1993).

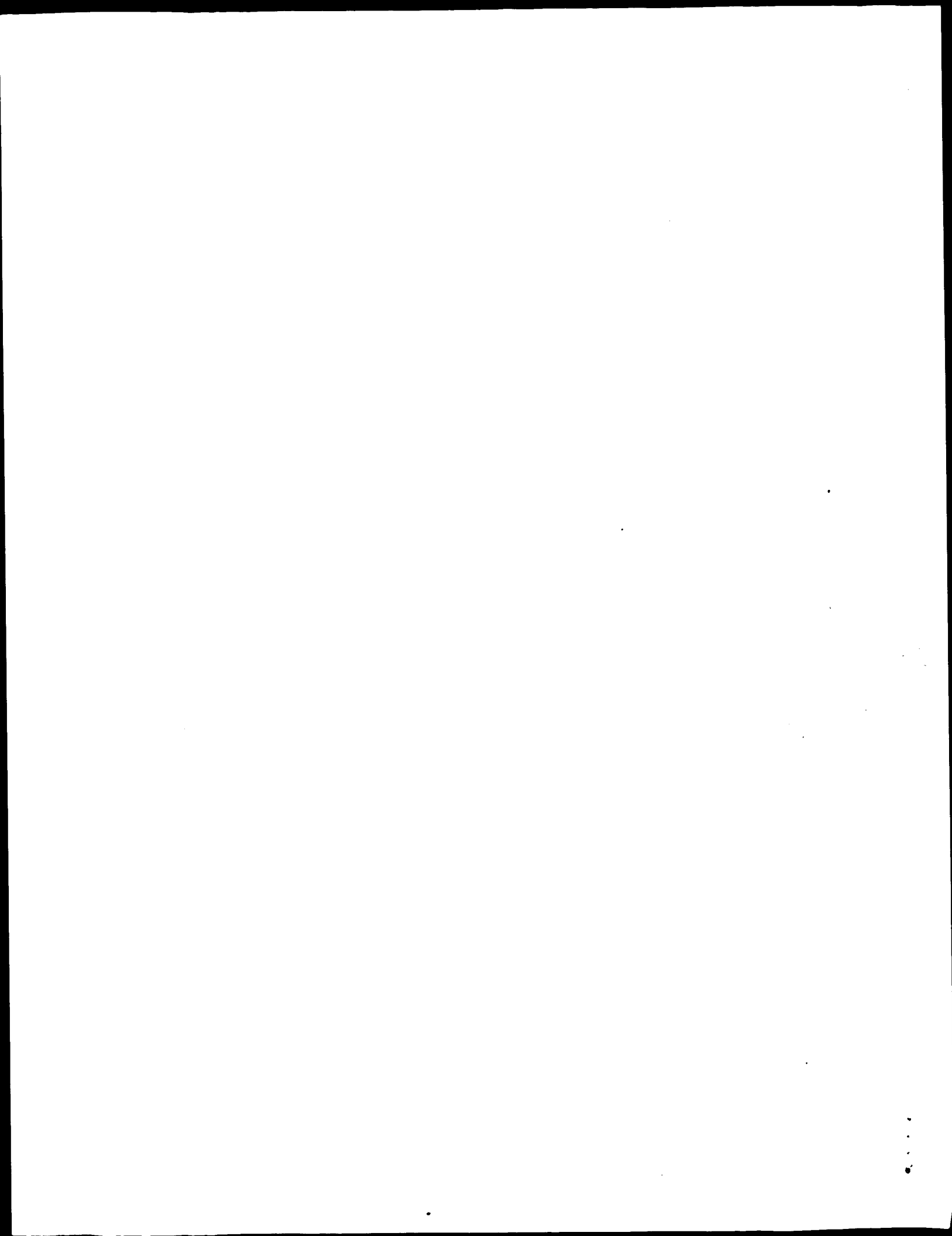
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD
 CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.

CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.



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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:27:31 ; Search time 22.45 Seconds
 (without alignments)
 49.392 Million cell updates/sec

Title: US-09-155-076-2
 Perfect score: 16
 Sequence: 1 DAEFRHDSGYEVHOK 16

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
 Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL12.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phase.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	82	4	Q16020
2	16	100.0	82	4	Q16019
3	16	100.0	82	4	Q16014
4	16	100.0	82	4	P78438
5	16	100.0	534	13	O93296
6	16	100.0	695	11	O60496
7	14	87.5	37	4	Q13778
8	10	62.5	699	13	O57394
9	7	43.8	747	13	Q91963
10	7	43.8	780	13	O73683
11	6	37.5	123	2	O53951
12	6	37.5	292	12	O85276
13	6	37.5	298	12	O85108
14	6	37.5	313	12	O85259
15	6	37.5	365	12	O9W605
16	6	37.5	379	12	O85257
17	6	37.5	380	1	O30016
18	6	37.5	447	10	O04340
19	6	37.5	453	1	O30322

20	6	37.5	533	11	O08569
21	6	37.5	704	13	Q90865
22	6	37.5	761	5	Q18468
23	6	37.5	976	12	O85104
24	6	37.5	1555	12	O85274
25	6	37.5	3051	12	O85265
26	5	31.2	58	1	O28675
27	5	31.2	76	2	P70764
28	5	31.2	105	2	O87879
29	5	31.2	112	2	O94629
30	5	31.2	123	1	Q9Y304
31	5	31.2	130	12	O9WY3
32	5	31.2	130	12	Q9WY3
33	5	31.2	132	3	P78948
34	5	31.2	141	1	Q9YDE5
35	5	31.2	142	5	O16896
36	5	31.2	174	2	O52573
37	5	31.2	178	5	Q17803
38	5	31.2	186	5	Q17303
39	5	31.2	195	2	O06241
40	5	31.2	195	12	O87073
41	5	31.2	196	2	O49789
42	5	31.2	208	5	O62213
43	5	31.2	209	2	O86679
44	5	31.2	230	4	Q13267
45	5	31.2	232	2	Q9ZHS1

ALIGNMENTS

RESULT 1

Q16020

ID Q16020; PRELIMINARY; PRT; 82 AA.

AC Q16020;

DT 01-NOV-1996 (TREMREL. 01, Created)

DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

DT 01-NOV-1999 (TREMREL. 12, Last annotation update)

DE BETA-AMYLLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236501.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61383; CAB32008.1; -.

DR HSSP; P05067; 1AML.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8882 MW; 55734509 CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 9.7e-12;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16

Db 18 DAEFRHDSGYEVHOK 33

RESULT 2

Q16019

ID Q16019; PRELIMINARY; PRT; 82 AA.

AC Q16019;

DT 01-NOV-1996 (TREMREL. 01, Created)

DT 01-NOV-1996 (TREMREL. 01, Last sequence update)

DT 01-NOV-1999 (TREMREL. 12, Last annotation update)

DE BETA-AMYLLOID PEPTIDE (FRAGMENT).

wed Sep 13 08:11:37 2000

us-09-155-076-2.rspt

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RX MEDLINE; 93236601.
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; CAB32007.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; 4C8B0B5E CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 3
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE BETA-AMYLID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RX MEDLINE; 93236601.
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; CAB31888.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 4
P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLID PEPTIDE) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

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SEQUENCE FROM N.A.
RX MEDLINE; 89392030.
RA JOHNSTONE E.M., CHANEY M.O., MOORE R.E., WARD K.E., NORRIS F.H.,
RA LITTLE S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RL similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RX SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE; 87120329.
RA TANZI R.E., GUSELLA J.F., WATKINS P.C., BRUNS G.A., GEORGE-HYSLOP P.,
RA VAN KEUREN M.L., PATTERSON D., PAGAN S., KURNIT D.M., NEVE R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RL linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RX SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE; 93035397.
RA KAMINO K., ORR H.T., PAYAMI H., WIJSMAN E.M., ALONSO M.E., PULST S.M.,
RA ANDERSON L., O'DAHL S., NEMENS E., WHITE J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RL kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51564.1; -.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSSP; P05067; 1AML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match 100.0%; Score 16; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
Db 17 DAEFRHDSGYEVHHQK 32

RESULT 5
O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RX SEQUENCE FROM N.A.
RA BARNES N.Y., LING L., YOSHIKAWA K., SCHWARTZ L.M., OPPENHEIM R.W.,
RA MILLIGAN C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for Caspase 3 in dying motoneurons.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1AML.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; 6F117D2F CRC32;

Query Match 100.0%; Score 16; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16

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Db 436 DAEFRHDSGYEVHHQK 451

RESULT 6
Q60496 PRELIMINARY; PRT; 695 AA.
ID O60496
AC O60496
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA BECK M., MOELLER D., BIGL V.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC (G(O).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; IAML.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 695 AA; 78701 MW; CE05C651 CRC32;

Query Match 100.0%; Score 16; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 5.8e-11; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 597 DAEFRHDSGYEVHHQK 612
|||||

RESULT 7
Q13778 PRELIMINARY; PRT; 97 AA.
ID Q13778
AC Q13778
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87130328.
RA GOLDGABER D., LERMAN M.I., MCBRIDE O.W., SAFFIOTTI U., GAJDUSEK D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; IAML.
FT NON_TER
SQ SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;

Query Match 87.5%; Score 14; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHHQK 16
Db 1 EFRHDSGYEVHHQK 14
|||||

RESULT 8

O57394 PRELIMINARY; PRT; 699 AA.
ID O57394
AC O57394
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE EL AMYLOID PRECURSOR PROTEIN 699.
GN EL APP699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Rajiformes; Narke.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ELECTRIC LOBE;
RA IJIMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,
RA SUZUKI T.;
RL Biochem. J. 0:0-0(1998).
DR EMBL; AB005544; BAA24230.1; -.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
SQ SEQUENCE 699 AA; 78879 MW; 11604C05 CRC32;

Query Match 62.5%; Score 10; DB 13; Length 699;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEVHHQK 16
Db 607 DSGYEVHHQK 616
|||||

RESULT 9
Q91963 PRELIMINARY; PRT; 747 AA.
ID Q91963
AC Q91963
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE APP747.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93129227.
RA OKADO H., OKAMOTO H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression."
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL; S52417; AAB24853.1; -.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PFAM; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PRINTS; PR00759; BASICTPASE.
KW Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;

Query Match 43.8%; Score 7; DB 13; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQK 16
Db 658 YEVHHQK 664
|||||

Wed Sep 13 08:11:37 2000

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RESULT 10
ID O73683 PRELIMINARY; PRT; 780 AA.
AC O73683;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ANKLOD PRECURSOR PROTEIN
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphs;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98252138.
RA VILLARD L., TASSONE F., CRNORAC-JURCEVIC T., CLANCY K., GARDINER K.;
RT "Analysis of pufferfish homologues of the At-rich human APP gene.";
RL Gene 210:17-24(1998).
DR EMBL; AF018165; AAC41275.1; -.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PFAM; PF00014; Runtz_SPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PRINTS; PR00759; BASICPTASE.
SQ SEQUENCE 780 AA; 88238 MW; 99DD89A8 CRC32;

Query Match 43.8%; Score 7; DB 13; Length 780;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 16
DB 691 YEVHHQ 697
|||||

RESULT 11
ID Q53951 PRELIMINARY; PRT; 123 AA.
AC Q53951;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE (FRAGMENT).
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyceinae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95231511.
RA PUTTIKUNT C., NIHARA T., YAMADA Y.;
RT "Cloning, nucleotide sequence, and transcriptional analysis of the
RT nusg gene of Streptomyces coelicolor A3(2), which encodes a putative
RT transcriptional antiterminator.";
RL Mol. Gen. Genet. 247:118-122(1995).
DR EMBL; D32254; BAA21035.1; -.
DR TRANSFERASE; Aminotransferase.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 12765 MW; 5394477B CRC32;

Query Match 37.5%; Score 6; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 DSGYEV 12
DB 93 DSGYEV 98
|||||

RESULT 12
ID Q85276 PRELIMINARY; PRT; 292 AA.
AC Q85276;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX GRIFFIN J.D., SHIEL P.S., BERGER P.H., THORNBURY D.W.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81435; AAA47185.1; -.
DR PFAM; PF00767; Poty_coat; 1.
KW Polyprotein.
FT NON_TER 1 1
FT CHAIN 1 25 NIB.
FT CHAIN 26 292 COAT PROTEIN.
SQ SEQUENCE 292 AA; 32945 MW; 8CB34E72 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 292;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
DB 20 YEVHHQ 25
|||||

RESULT 13
ID Q85108 PRELIMINARY; PRT; 298 AA.
AC Q85108;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CAPSID PROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NNP;
RA D'AQUINO L., DALWAY T., BURGYN J., RAGOZZINO A., SCALA F.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10378; AAA19172.1; -.
DR PFAM; PF00767; Poty_coat; 1.
FT NON_TER 1 1
FT NON_TER 298 298
SQ SEQUENCE 298 AA; 33459 MW; 93324303 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 298;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEVHHQ 15
DB 27 YEVHHQ 32
|||||

RESULT 14
ID Q85259 PRELIMINARY; PRT; 313 AA.
AC Q85259;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)

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DE ORF (FRAGMENT).
 OS Potato virus Y.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-NECROTIC (PVY-T);
 RC HIDAKA M.;
 RA Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
 RL EMBL; D12570; BAA02120.1;
 DR PFAM; PF00767; Poty_coat; 1.
 KW Coat protein. 1
 FT NON_TER 1
 FT CHAIN 47 313 COAT PROTEIN.
 SQ SEQUENCE 313 AA; 35372 MW; 453E75C2 CRC32;

Query Match 37.5%; Score 6; DB 12; Length 313;
 Best Local Similarity 100.0%; Pred. No. 9.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

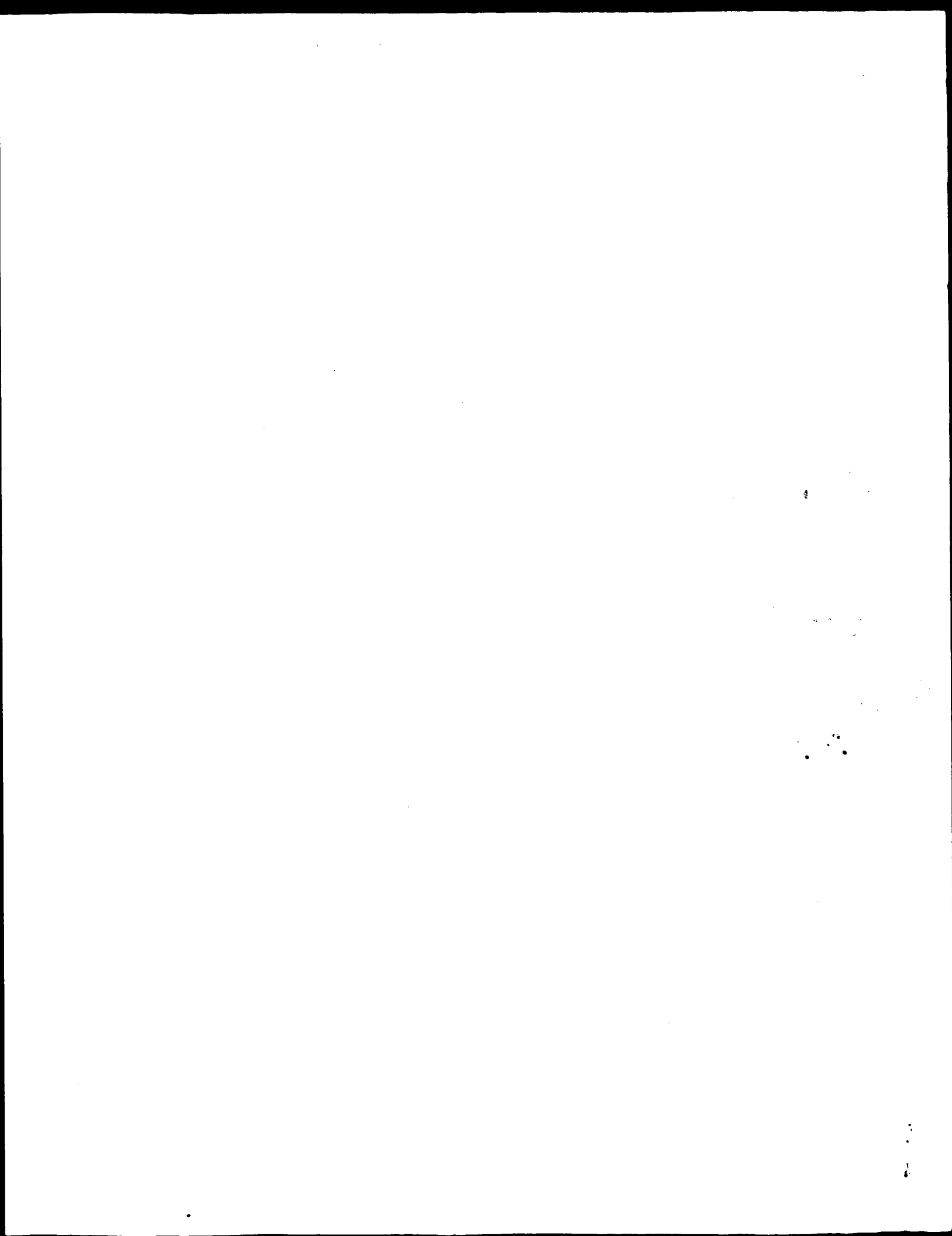
QY 10 YEYVHHQ 15
 |11111
 DB 41 YEYVHHQ 46

RESULT 15
 Q9WG05 PRELIMINARY; PRT; 365 AA.
 AC Q9WG05;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE POLYPROTEIN (FRAGMENT).
 OS Potato virus Y.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ORDINARY, O;
 RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;
 RT "N-terminal serology and sequence relationships indicate that a
 RT potyvirus from eggplant, Solanum melongena L., is a strain of potato
 RT virus Y."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF118153; AAD24563.1;
 KW Polyprotein. 1
 FT NON_TER 1
 SQ SEQUENCE 365 AA; 41418 MW; F3CF9EBD CRC32;

Query Match 37.5%; Score 6; DB 12; Length 365;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 YEYVHHQ 15
 |11111
 DB 93 YEYVHHQ 98

Search completed: September 13, 2000, 02:27:32
 Job time: 174 sec



OM of: US-09-155-076-2 to: EST:* out_format : pfs

Date: Sep 13, 2000 3:35 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-DB=EST -OEXT=fastap -SUFFIX=rst -GAPOP=4.500 -GAPEXT=0.050
-MINWATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-LOOPEXT=0.050 -GAPOP=60.000 -GAPEXT=60.000 -GAPOP=6.000
-DELEXT=7.000 -GAPOP=60.000 -GAPEXT=60.000 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15
-MODE=LOCAL -OUTEXT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000
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-WAIT -THREADS=1
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: EST*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 889.020000

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WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:

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gb_est4:AA379017	-	16.00	339.24	4.6e-10	277	AA379017 RC3-HT0330-241099-012
gb_est27:AA390926	-	16.00	339.22	4.6e-10	278	AA390926 QV-BT202-070599-188 BT
gb_est5:AA303751	+	16.00	338.85	4.8e-10	297	AA303751 EST16434 Aorta endothel
gb_est47:AF06018	+	16.00	338.70	4.9e-10	305	F06018 HSC00A101 normalized inf
gb_est44:AA580695	-	16.00	338.68	4.9e-10	306	AA580695 RC4-LT0011-100100-012
gb_est26:AA390258	-	16.00	338.17	5.2e-10	335	AA390258 QV-BT009-101198-075 BT
gb_est5:AA322074	-	16.00	338.12	5.3e-10	338	AA322074 EST24653 Cerebellum II
gb_est5:AA304003	+	16.00	338.12	5.3e-10	338	AA304003 QV-BT009-101198-074 BT
gb_est52:TA49906	+	16.00	337.86	5.4e-10	354	AA304003 EST16883 Aorta endothel
gb_est51:RI9709	+	16.00	337.42	5.8e-10	383	TA9906 ya99b06.r1 Stratagene pl
gb_est2:AA134479	-	16.00	337.19	5.9e-10	399	RI9709 YG35f04.r1 Soares infant
gb_est16:AA124771	-	16.00	336.95	6.1e-10	417	AA134479 zol0c04.r1 Stratagene
gb_est44:AW601576	+	16.00	336.39	6.6e-10	461	AA124771 am61h12.x1 Johnston fi
gb_est5:R25913	+	16.00	336.29	6.7e-10	469	AW601576 QV3-BT0381-270100-073
gb_est3:AA218652	+	16.00	336.10	6.8e-10	485	R25913 YG56c07.r1 Soares infant
gb_est4:AA602193	+	16.00	335.81	7.1e-10	511	AA218652 zq14d12.s1 Stratagene
gb_est45:AW673480	+	16.00	335.48	7.4e-10	542	AW602193 PM2-BT0546-210100-004
gb_est2:AA082598	+	16.00	334.86	8.0e-10	606	AW673480 ba54e09.V3 NIH MGC_10
gb_est2:AA081859	+	16.00	334.81	8.1e-10	611	AA081859 zn25c07.r1 Stratagene
gb_est28:AA980795	+	16.00	334.72	8.2e-10	621	AA081859 zn25g07.r1 Stratagene
gb_est44:AW581403	+	16.00	334.45	8.4e-10	652	AA980795 pat.pk0033.f8.f chickc
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gb_est1:AA032972	+	14.00	297.03	1.0e-07	286	AW607890 RC0-HT0505-180100-011
gb_est1:AA034297	+	14.00	296.92	1.0e-07	289	AA032972 zk07c09.r1 Soares pred
gb_est4:AW608486	+	14.00	294.68	1.4e-07	440	AA034297 zk20a06.r1 Soares pred
gb_est41:AW626065	-	14.00	292.54	1.8e-07	539	AW608486 RC0-LT0070-170100-031
gb_est54:W26339	-	13.00	270.83	1.4e-06	264	AA362065 PM2-CT0265-281099-004
gb_est5:AA299326	+	12.00	253.41	3.0e-05	724	W26339 26B3 Human retina cdna
gb_est44:AW581394	-	12.00	250.42	4.8e-05	381	AA299326 EST11904 Uterus tumor
gb_est44:AW608448	+	12.00	250.10	4.2e-05	650	AW581394 RC0-LT0070-070100-011
gb_est54:W26191	+	11.00	250.10	4.2e-05	688	AW608448 RC0-LT0070-170100-031
gb_est4:AW608455	+	11.00	239.84	0.0006	602	W26191 22B11 Human retina cdna
gb_est47:DS1546	+	10.00	211.31	0.0061	386	AW608455 RC0-LT0070-170100-031
gb_est53:TS6402	+	10.00	210.57	0.0067	441	DS1546 HM042F12B Clontech huma
gb_est41:AW393653	-	10.00	210.15	0.0071	475	T64402 QY0906.r1 Stratagene lu
gb_est54:W27250	-	10.00	209.64	0.0076	520	AW393653 RC5-ST0317-161299-011
gb_est54:W26650	-	10.00	206.48	0.0113	915	W27250 24G5 Human retina cdna

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gb_est54:W27265 + 9.00 187.71 0.1258 613 ! W27265 24f1 Human retina cdn
gb_est54:W27702 + 9.00 187.59 0.1277 626 ! W27702 36g11 Human retina cd
gb_est44:AW607850 + 9.00 187.58 0.1280 628 ! AW607850 RC0-HT0505-010200-0
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seq_documentation_block:

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DEFINITION EST99048 Thyroid Homo sapiens CDNA 5' end similar to amyloid, A4
beta subunit, mRNA sequence.
ACCESSION AA385402
VERSION AA385402.1 GI:2037720
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)

REFERENCE

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fink,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palances,R.F., McDonald,L.A., Nguyen,D.T., Peilgrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

MEDLINE

COMMENT

Other_ESTs: THCL72078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699036

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M3 Reverse.

Location/Qualifiers

1. 246

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/db_xref="taxon:9606"

/clone_lib="Thyroid"

/dev_stage="adult"

/note="Organ: thyroid gland; Vector: pBluescript SK-;

Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 70 a 48 c 68 g 58 t 2 others

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Quality: 16.00 Length: 16

Ratio: 1.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

LOCUS	AI909276	278 bp	mrna	EST	30-MAR-2000
DEFINITION	OV-BT202-070599-188	BT202	Homo sapiens	cdna	mrna sequence.
ACCESSION	AI909276				
VERSION	AI909276.1	GI:6499956			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., Geolvelira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)		3491-3496	(2000)
COMMENT	On Jan 19, 1998 this sequence version replaced gi:2284565.				
	Contact: Simpson A.J.G.				
	Laboratory of Cancer Genetics				
	Ludwig Institute for Cancer Research				
	Rua Prof. Antonio Prudente 109, 4 andar,			01509-010, Sao Paulo-SP, Brazil	
	Tel: +55-11-2704922				
	Fax: +55-11-2707001				
	Email: asimpson@ludwig.org.br				
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?ti=QVst2-QV-BT202-188.html&t3=070599&t4=1)				
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	/clone_lib="BT202"				
	/sex="female"				
	/dev_stage="Adult"				
	/note="Organ: breast; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	71 a 79 c 54 g 74 t				
ORIGIN					
alignment_scores:	Quality: 16.00	Length: 16			
	Ratio: 1.000	Gaps: 0			
Percent Similarity:	100.000	Percent Identity:	100.000		
alignment_block:					
US-09-155-076-2 x AI909276/rev					
Align seg 1/1 to reverse of: AI909276	from: 1	to: 278			
	1	AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys	16		
	207	GATGAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA	160		
seq_name:	gb_est5:AA303751				
seq_documentation_block:					
LOCUS	AA303751	297 bp	mrna	EST	18-APR-1997
DEFINITION	EST16434	Aorta endothelial cells, TNF alpha-treated	Homo sapiens		
	CDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.				
ACCESSION	AA303751				
VERSION	AA303751.1	GI:1956103			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., Geolvelira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)		3491-3496	(2000)
COMMENT	On Jan 19, 1998 this sequence version replaced gi:2284565.				
	Contact: Simpson A.J.G.				
	Laboratory of Cancer Genetics				
	Ludwig Institute for Cancer Research				
	Rua Prof. Antonio Prudente 109, 4 andar,			01509-010, Sao Paulo-SP, Brazil	
	Tel: +55-11-2704922				
	Fax: +55-11-2707001				
	Email: asimpson@ludwig.org.br				
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?ti=RC3t2-RC3-HT0230-241099-012-cl2&t3=1999-10-24&t4=1)				
	Seq primer: puc 18 forward				
	High quality sequence stop: 277.				
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	/dev_stage="Adult"				
	/note="Organ: head_neck; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
BASE COUNT	70 a 79 c 51 g 77 t				
ORIGIN					
alignment_scores:	Quality: 16.00	Length: 16			
	Ratio: 1.000	Gaps: 0			
Percent Similarity:	100.000	Percent Identity:	100.000		

KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 297)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitchugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Keiley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT 12140200
 On Sep 29, 1997 this sequence version replaced gi:1520591.
 Other_ESTs: TNC172078
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M3 Reverse.

FEATURES
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 /dev_stage="adult"
 /note="Organ: aorta; Vector: pBluescript SK-; Site_1:
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alignment_scores:
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 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
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 217 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 264
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 seq_documentation_block:
 LOCUS F06018 305 bp mRNA EST 19-FEB-1995
 DEFINITION HSCOUA101 normalized infant brain cDNA Homo sapiens cDNA clone

alignment_scores:
 Quality: 16.00 Length: 16
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 seq_name: gb_est47:F06018
 seq_documentation_block:
 LOCUS F06018 305 bp mRNA EST 19-FEB-1995
 DEFINITION HSCOUA101 normalized infant brain cDNA Homo sapiens cDNA clone

ACCESSION
VERSION F06018.1
KEYWORDS GI:569834
SOURCE EST.
ORGANISM Homo sapiens

REFERENCE
AUTHORS 1 (bases 1 to 305)
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 305)
 Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
 Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
 Lorenzo,F., Mitcheil,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
 Sebastiani,Kabatchis,C. and Tessier,A.
TITLE IMAGE: molecular integration of the analysis of the human genome
 and its expression
 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
 95277534
JOURNAL On May 20, 1999 this sequence version replaced gi:4878117.
MEDLINE Contact: Genethon
COMMENT Genexpress:Genethon
 Genethon Centre de recherche sur le Genome Humain
 1, rue de l'Internationale, Bp60 91002 EVRY Cedex, FRANCE
 Tel: 33169472800
 Fax: 33160778698
 Email: genexpress@genethon.fr
 Single read.

FEATURES
 source
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 /dev_stage="3 months old"
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 Site_2: NotI; sex:Female; dev_stage=3 months old;
 isolate=muscular atrophy patient; tissue_type=total
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 cloned 5' -> 3' into the HindIII -> NotI sites of the
 lafmid BA vector. Clone library from B.Soaers, Psychiatry
 Dept. Columbia University, USA. Normalization_method:
 Bento Soares, P.N.A.S in press"
 BASE COUNT 88 a 65 c 80 g 71 t 1 others
 ORIGIN

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 Percent Similarity: 100.000 Percent Identity: 100.000
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 3 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 50
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 seq_documentation_block:
 LOCUS AW580695 306 bp mRNA EST 16-MAR-2000
 DEFINITION RC4-LT0011-100100-012-cl1 LT0011 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW580695
 VERSION AW580695.1
 KEYWORDS GI:7255744
 EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 306)
HCGP <http://www.ludwig.org.br/ORESPE>.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
On Jan 6, 2000 this sequence version replaced gi:6676947.

JOURNAL

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC4&t2=RC4-LT0011-100100-012-cl1&t3=2000-01-10&t4=1>)

JOURNAL

COMMENT

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High quality sequence start: 6
High quality sequence stop: 306.
Location/Qualifiers
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/clone_lib="LT0011"
/dev_stage="Adult"
/note="Organ: leiomyos; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
72 a 80 c 65 g 89 t

BASE COUNT

ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AW580695/rev ..

Align seg 1/1 to reverse of: AW580695 from: 1 to: 306

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seq_documentation_block:
LOCUS AI902528 335 bp mRNA EST 30-MAR-2000
DEFINITION QV-BT009-101198-075 BT009 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI902528
VERSION AI902528.1 GI:6492915
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 335)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
On May 18, 1998 this sequence version replaced gi:3138510.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=QV&t2=QV-BT009-075.html&t3=101198&t4=1>)

FEATURES

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/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
77 a 89 c 76 g 93 t

BASE COUNT

ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
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alignment_block:
US-09-155-076-2 x AI902528/rev ..

Align seg 1/1 to reverse of: AI902528 from: 1 to: 335

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seq_name: gb_est5:AA322074

seq_documentation_block:
LOCUS AA322074 338 bp mRNA EST 19-APR-1997
DEFINITION EST24653 Cerebellum II Homo sapiens cDNA 5' end similar to amyloid,
A4 beta subunit, mRNA sequence.
ACCESSION AA322074
VERSION AA322074.1 GI:1974399
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 338)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
White, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
Bult, C.J., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glock, A., Gnehm, C.D., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palances, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

TITLE
JOURNAL
MEDLINE
COMMENT

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
 Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
 Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)

Other_ESTS: THC172078
Contact: Kerlavage, AR
Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse

FEATURES

source
 1. .338
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):122569"
 /db_xref="taxon:9606"
 /clone.lib="Cerebellum II"
 /tissue_type="cerebellum"
 /dev_stages="adult"
 /note="Organ: brain; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
BASE COUNT 86 a 78 c 95 g 79 t
ORIGIN

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AA322074 ..
 Align seg 1/1 to: AA322074 from: 1 to: 338

1 AspalagluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
 |||||
 210 GATCGAGATTCCGACATGCTCAGGATATGAGTTTCATCATCAAAA 257

seq_name: gb_est26:AI902529

seq_documentation_block:
LOCUS AI902529 338 bp mRNA EST 30-MAR-2000
DEFINITION OV-BT009-101198-074 BT009 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI902529
VERSION AI902529.1 GI:6492916
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
 Dias Neto,E., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
 Nagai,M.A., Goldman,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.Y. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE
JOURNAL
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 On Oct 30, 1998 this sequence version replaced gi:3814489.

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?tl-QV&t2-QV-BT009-074.html>)
seq primer: puc 18 forward.

FEATURES

source
 1. .338
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone.lib="BT009"
 /sex="female"
 /dev_stage="Adult"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
BASE COUNT 78 a 89 c 76 g 95 t
ORIGIN

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AI902529/rev ..
 Align seg 1/1 to reverse of: AI902529 from: 1 to: 338
 1 AspalagluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
 |||||
 315 GATCGAGATTCCGACATGCTCAGGATATGAGTTTCATCATCAAAA 268

seq_name: gb_est5:AA304003

seq_documentation_block:
LOCUS AA304003 354 bp mRNA EST 18-APR-1997
DEFINITION EST16883 Aorta endothelial cells, TNF alpha-treated Homo sapiens
 cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.
ACCESSION AA304003
VERSION AA304003.1 GI:1956491
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Frichman,J.L., Georghagen,N.S.,
 Glodok,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligriano,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,

Wed Sep 13 08:11:37 2000

On Nov 2, 1998 this sequence version replaced gi:3828645.

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 384.

FEATURES

Source

1..383
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:490676"
/db_xref="taxon:9606"
/clone="IMAGE:69779"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: Placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT

ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x T49906

Align seg 1/1 to: T49906 from: 1 to: 383

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
61 GATGCGAATTCCGACATGACTCAGGATATGAAAGTTTCATCATCAAAA 108

seq_name: gb_est51:R19709

seq_documentation_block:

LOCUS R19709 399 bp mRNA EST 17-APR-1995
DEFINITION Y935f04.r1 Soares infant brain LNTB Homo sapiens cDNA clone
IMAGE:34389 5' similar to gb:X06989.rnal ALZHEIMER'S DISEASE
AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

R19709

R19709.1 GI:774343

VERSION

EST.

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 399)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

On Jan 19, 1998 this sequence version replaced gi:2284625.

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE

COMMENT

On Jan 17, 1998 this sequence version replaced gi:1900069.

Other_ESTs: THCL172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..354

/organism="Homo sapiens"

/db_xref="ATCC (inhost):115766"

/db_xref="taxon:9606"

/clone_lib="Aorta endothelial cells, TNF alpha-treated"

/cell_type="endothelial cell"

/dev_stage="adult"

/note="Organ: aorta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

EcoRI; Site_2: XhoI"

102 a 80 c 92 g 78 t 2 others

BASE COUNT

ORIGIN

alignment_scores:
Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AA304003

Align seg 1/1 to: AA304003 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
10 GATGCGAATTCCGACATGACTCAGGATATGAAAGTTTCATCATCAAAA 57

seq_name: gb_est52:T49906

seq_documentation_block:

LOCUS T49906 383 bp mRNA EST 06-FEB-1995
DEFINITION ya99b06.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone
IMAGE:69779 5' similar to gb:X06989.rnal ALZHEIMER'S
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.

ACCESSION

T49906

T49906.1 GI:651766

VERSION

EST.

KEYWORDS

human.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 383)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favellio, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.

and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

Insert Size: 1369
 High quality sequence stops: 214 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1369 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stops: 214.

FEATURES

Location/Qualifiers
 1..399
 /organism="Homo sapiens"
 /db_xref="GDB:406736"
 /db_xref="taxon:9606"
 /clone="IMAGE:34389"
 /clone.lib="Soares infant brain 1N1B"
 /sex="female"
 /dev.stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
 I; Site_2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(GT) primer [5'
 AACGCGAGATTGCGCGCCGAGCAATTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lfamid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 104 a 85 c 106 g 94 t 10 others
 ORIGIN

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-2 x R19709 ..

Align seg 1/1 to: R19709 from: 1 to: 399

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||
 219 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 266

seq_name: gb_est2:AA134479

seq_documentation_block:
 LOCUS AA134479 417 bp mRNA EST 23-DEC-1997
 DEFINITION z010904.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
 cDNA clone IMAGE:567318 5' similar to gb:X06989_rnal ALZHEIMER'S
 DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA134479
 VERSION AA134479.1 GI:1692245

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 417)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Scheinberg, K., Soares, M.B., Tan, F., Thierly-Meg, J.,
 Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
 and Marra, M.

TITLE Generation and analysis of 289,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 9704478

COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

WARNING: there is evidence that suggests that the 384-well parent
 plate of this clone contains both human and mouse derived clones.
 Thus, the origin of this clone is uncertain. This caution should be
 kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1384 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stops: 394.

FEATURES

Location/Qualifiers
 1..417
 /organism="Homo sapiens"
 /db_xref="GDB:459171"
 /db_xref="taxon:9606"
 /clone="IMAGE:567318"
 /clone.lib="Stratagene neuroepithelium NT2RAMI 937234"
 /dev.stage="Ntera-2/RA+MI neuroepithelial cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
 (Ntera-2/ci.D1) precursor cells induced with Retinoic
 Acid for 1 week, followed by 3 weeks in mitotic inhibitors
 (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR
 Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3"

BASE COUNT 110 a 93 c 117 g 95 t 2 others
 ORIGIN

alignment_scores:
 Quality: 16.00 Length: 16
 Ratio: 1.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-2 x AA134479 ..

Align seg 1/1 to: AA134479 from: 1 to: 417

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||
 159 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 206

seq_name: gb_est16:AI124771

seq_documentation_block:
 LOCUS AI124771 461 bp mRNA EST 11-SEP-1998
 DEFINITION am1h12.x1 Johnston frontal cortex Homo sapiens cDNA clone
 IMAGE:1540103 3' similar to gb:X06989_rnal ALZHEIMER'S DISEASE
 AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI124771

VERSION AI124771.1 GI:3593285

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 461)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

CONTACT: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 423.

FEATURES

source

Location/Qualifiers
1. .461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1540103"
/clone_lib="Johnston frontal cortex"
/sex="male"
/tissue_type="pooled frontal lobe"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site:1:
ECORI; Stanley NeuroPathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.
Random + oligo-dT primed into EcoRI site of ZAP II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
njewelchlink.welch.jhu.edu]."
BASE COUNT 101 a 123 c 110 g 126 t 1 others
ORIGIN

alignment_scores:

Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x A1124771/rev ..

Align seg 1/1 to reverse of: A1124771 from: 1 to: 461

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
314 GATGAGAATTCGACATGACTCAGGATGATGAGATTCATCATCAAAA 267

seq_name: gb_est44:AW601576

seq_documentation_block:

LOCUS AW601576 469 bp mRNA EST 23-MAR-2000
DEFINITION QV3-BT0381-270100-073-f06 BT0381 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW601576
VERSION AW601576.1 GI:7306315
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 469)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT On Jan 6, 2000 this sequence version replaced gi:6677550.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3st2-QV3-BT0381-270100-073-f06st3-2000-01-27st4-1>)

Seq primer: puc 18 forward

High quality sequence start: 111

High quality sequence stop: 469.

FEATURES

source

Location/Qualifiers
1. .469

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0381"
/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
136,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 128 a 120 c 117 g 104 t
ORIGIN

alignment_scores:

Quality: 16.00 Length: 16
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AW601576 ..

Align seg 1/1 to: AW601576 from: 1 to: 469

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
422 GATGAGAATTCGACATGACTCAGGATGATGAGATTCATCATCAAAA 469

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:21:36 ; Search time 17.65 seconds
(without alignments)
21.472 Million cell updates/sec

Title: US-09-155-076-2
Perfect score: 92
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	100.0	16	1 R60371	Beta-amyloid (1-16)
2	92	100.0	16	1 W35344	Human beta-amyloid
3	92	100.0	21	1 W08361	Beta-secretase sub
4	92	100.0	22	1 R07753	Beta-amyloid prot
5	92	100.0	28	1 P90381	Synthetic A4 amylo
6	92	100.0	28	1 R54702	Beta-amyloid fragm
7	92	100.0	28	1 R60368	Beta-amyloid (1-28
8	92	100.0	28	1 W01413	Beta/A4-amyloid pe
9	92	100.0	28	1 W01414	Beta/A4-amyloid pe
10	92	100.0	28	1 R64170	A4-O(1-28) a parti
11	92	100.0	28	1 R64172	A4-B(1-28) a parti
12	92	100.0	28	1 W81467	Synthetic amyloid
13	92	100.0	30	1 W81468	Synthetic amyloid
14	92	100.0	33	1 W08359	Beta-secretase sub
15	92	100.0	33	1 W81469	Synthetic amyloid
16	92	100.0	33	1 W98002	Amyloid precursor
17	92	100.0	35	1 W02335	Beta-amyloid pepti
18	92	100.0	35	1 W47228	Beta-amyloid pepti
19	92	100.0	35	1 W89355	Beta-amyloid pepti
20	92	100.0	35	1 W89359	Beta-amyloid pepti
21	92	100.0	36	1 W81471	Synthetic amyloid
22	92	100.0	38	1 R60362	Beta-amyloid (1-38
23	92	100.0	38	1 W92722	Human tachykinin a
24	92	100.0	39	1 R60363	Beta-amyloid (1-39
25	92	100.0	39	1 W81472	Synthetic amyloid
26	92	100.0	40	1 R33191	Beta-amyloid pepti
27	92	100.0	40	1 R60364	Beta-amyloid (1-40
28	92	100.0	40	1 W23335	Amyloid beta pepti
29	92	100.0	40	1 W37507	Amyloid beta prote
30	92	100.0	40	1 W47232	Beta-amyloid pepti
31	92	100.0	40	1 W47226	Beta-amyloid pepti
32	92	100.0	40	1 W81473	Synthetic amyloid
33	92	100.0	40	1 W92723	Human tachykinin a

34	92	100.0	40	1 W95584	Wild type aggregat
35	92	100.0	41	1 R22206	Alzheimer's amyloi
36	92	100.0	41	1 R60365	Beta-amyloid (1-41
37	92	100.0	41	1 R65283	Beta amyloid pepti
38	92	100.0	42	1 R20330	Sequence of A99 (b
39	92	100.0	42	1 R33192	Beta-amyloid pepti
40	92	100.0	42	1 R60366	Beta-amyloid (1-42
41	92	100.0	42	1 R65285	Beta amyloid pepti
42	92	100.0	42	1 R65286	Beta amyloid pepti
43	92	100.0	42	1 R65287	Beta amyloid pepti
44	92	100.0	42	1 R65288	Beta amyloid pepti
45	92	100.0	42	1 R94591	Alzheimer amyloid

ALIGNMENTS

RESULT 1
R60371 ID R60371 standard; peptide; 16 AA.
AC R60371; 1995 (first entry)
DT 15-MAR-1995
DE Beta-amyloid (1-16).
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
OS Homo sapiens.
PN W09417197-A.
PD 04-AUG-1994.
PF 24-JAN-1994; J00089.
PR 25-JAN-1993; JP-010132.
PR 05-FEB-1993; JP-019035.
PR 16-NOV-1993; JP-286985.
PR 28-DEC-1993; JP-334773.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Kitada C, Odaoka A, Suzuki N;
DR WPI; 94-264110/32.
PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease
PT Claim 7; Page 85; 116pp; Japanese.
PS CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.
SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2
W35344 ID W35344 standard; peptide; 16 AA.
AC W35344;
DT 17-APR-1998 (first entry)
DE Human beta-amyloid precursor 16-mer peptide.
KW Beta-amyloid precursor polypeptide; acetylcholinesterase; AChE;
KW neuronal degeneration; Parkinson's disease; Alzheimer's disease;
KW stroke; cancer; calcium channel modulator; antibody; inhibitor.
OS Homo sapiens.
PN W09735962-AI.
PD 02-OCT-1997.
PF 21-MAR-1997; G00796.
PR 22-MAR-1996; GB-006040.

PA (ISIS-) ISIS INNOVATION LTD.
PI Greenfield SA, Vaux DJ;
DR WPI; 97-489626/45.
PT Peptide(s) from acetylcholine esterase which open calcium channels -
PT used for treating disorders of the central nervous system, cancer
PT and stroke
PS Claim 3; Page 20; 27pp; English.
CC This 16-mer peptide is present in a region of the beta-amyloid precursor
CC polypeptide. This region lies at the amino acid terminus of the 42
CC residue peptide which accumulates in Alzheimer's disease. The 16-mer
CC has at least 70% homology with the beta-amyloid precursor. This peptide
CC is known to act alone or in synergism with a fragment of
CC acetylcholinesterase (W35340-W35343) to contribute to neuronal
CC degeneration. Compounds that inhibit the biological activity of the
CC novel peptides, and antibodies, can be used to control cytoplasmic
CC calcium ion currents in vivo, and are useful for treating disorders of
CC the central nervous system (e.g. Parkinson's and Alzheimer's diseases),
CC stroke and cancer.
SQ Sequence 16 AA;

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 3

ID W08361 standard; peptide; 21 AA.
AC W08361;
DT 05-SEP-1997 (first entry)
DE Beta-secretase substrate #3.
KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
OS Synthetic.
PN W09640885-A2.
PD 19-DEC-1996.
PF 07-JUN-1996; U09985.
PR 07-JUN-1995; US-485152.
PR 07-JUN-1995; US-480498.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI Mcconlogue LC, Sinha S, Tan H;
DR WPI; 97-052304/05.
PT Beta-secretase which specifically cleaves beta-amyloid precursor
PT protein - useful to screen for inhibitors useful in treatment of
PT Alzheimer's disease
PS Disclosure; page 45; 92pp; English.
CC W08359-W08362 represent substrates for the enzyme of the invention. The
CC enzyme of the invention is beta-secretase, and specifically cleaves
CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
CC is thought to occur via cleavage between residues 16 and 17 of the
CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
CC is thought to occur by beta-secretase cleavage of beta-APP.
CC Beta-secretase activity can be detected and measured using a method of
CC the invention, which detects at least one of the beta-secretase cleavage
CC products formed on cleavage. The method can be used to determine whether
CC a test substance inhibits proteolytic cleavage, by beta-secretase, of
CC beta-APP. Compounds effective to at least partially inhibit
CC beta-secretase activity can be used to inhibit cleavage of beta-APP in
CC cells or mammalian hosts. Isolation and purification of beta-secretase
CC will permit chemical modelling of a critical event in the pathology of
CC Alzheimer's disease.
SQ Sequence 21 AA;

Query Match 100.0%; Score 92; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
DB 6 DAEFRHDSGYEVHHQK 21

RESULT 4

ID R07753 standard; protein; 22 AA.
AC R07753;
DT 22-FEB-1991 (first entry)
DE Beta-amyloid protein, SCVAP2.
KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease;
KW beta-amyloid precursor; amyloid plaques.
OS synthetic.
PN W09012871-A.
PD 01-NOV-1990.
PF 13-APR-1989; US-338983.
PR 14-APR-1989; US-338983.
PA (REME-) RES FOUND MENTAL HY.
PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;
DR WPI; 90-348474/46.
PT Cerebrovascular amyloid protein-specific monoclonal antibody
PT SV17-6E10 - for immunoassay of peptide whose levels are raised in
PT Down's syndrome or Alzheimer's disease patients
PS Example 4; page 11; 24pp; English.
CC This peptide is used in a "Double Ab Sandwich Immunoassay" to
CC detect beta-amyloid protein. SV17-6E10 MAb(capture Ab) is used
CC to coat microtitre plate wells. The plate is then washed (dist-
CC illed water), coated with PBS(rgb) and this (SCVAP2) protein is
CC added. The plate is washed and a 2nd Ab (detection Ab), MAB 468-
CC This double Ab sandwich ELISA test is a highly sensitive and
CC accurate detection system for the beta-amyloid protein.
CC See also R07752.
SQ Sequence 22 AA;

Query Match 100.0%; Score 92; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 5

ID P90381 standard; protein; 28 AA.
AC P90381;
DT 1-NOV-1989 (first entry)
DE Synthetic A4 amyloid peptide
KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;
KW immunoassays; antibodies.
OS Synthetic
PN W08906242-A.
PD 13-JUL-1989.
PF 11-OCT-1988; U03590.
PR 08-OCT-1987; US-105751.
PA (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.
PI Majocha R, Marotta CA, Zain S;
DR WPI; 89-220551/30.
PT Antibodies to A4 amyloid polypeptide
PT - used in immunoassays and for imaging of A4 amyloid
PT in Alzheimer's diseased patients.
PS Claim 1; page 27; 30pp; English.
CC Synthetic A4 amyloid polypeptide (see also P90382, P90383).
CC Used as immunogen, (un)coupled, or to produce antibodies. Used in
CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.
SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 6
 R54702
 ID R54702 standard; peptide; 28 AA.
 AC R54702;
 DT 15-DEC-1994 (first entry)
 DE Beta-amyloid fragment (1-28).
 KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
 OS Homo sapiens.
 PN W09409364-A.
 PD 28-APR-1994.
 PF 13-OCT-1993; U09772.
 PR 13-OCT-1992; US-959251.
 PA (UYDU-) UNIV DUKE.
 PI Strittmatter WJ;
 DR WPI: 94-15148/16;
 PT Immobilised beta-amyloid protein or fragments - used in assays for obtaining prods for use in the diagnosis and treatment of PT disorders such as Alzheimer's disease.
 PS Claim 4: Page 28; 49pp; English.
 CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp. the peptides given in R54702-03) immobilised on a solid support can be used to detect cpds. which bind to BAP. Binding of proteins in CC human cerebrospinal fluid proteins were shown to bind to beta-amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28) CC was used as control.
 SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 7
 R60368
 ID R60368 standard; peptide; 28 AA.
 AC R60368;
 DT 15-MAR-1995 (first entry)
 DE Beta-amyloid (1-28).
 KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid; anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
 OS Homo sapiens.
 PN W09417197-A.
 PD 04-AUG-1994.
 PF 24-JAN-1994; J00089.
 PR 25-JAN-1993; JP-010132.
 PR 05-FEB-1993; JP-019035.
 PR 16-NOV-1993; JP-286985.
 PR 28-DEC-1993; JP-334773.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Kitada C, Odaka A, Suzuki N;
 DR WPI: 94-264110/32;
 PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as PT Alzheimer's disease
 PS Claim 7: Page 84; 116pp; Japanese.
 CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 CC from the C-terminal portion. The antibodies are useful for assaying

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 92; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 8
 W01413
 ID W01413 standard; Protein; 28 AA.
 AC W01413;
 DT 20-JAN-1997 (first entry)
 DE Beta/A4-amyloid peptide residues 1-28.
 KW Beta/A4-amyloid peptide; tissue plasminogen activator;
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
 KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
 KW hemorrhage.
 OS Homo sapiens.
 PN W09615799-A1.
 PD 30-MAY-1996.
 PF 22-NOV-1995; U15007.
 PR 22-NOV-1994; US-347144.
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PI Anderson S;
 DR WPI: 96-268332/27;
 PT Use of agents which bind beta-amyloid peptide - for diagnosis, prevention and treatment of vascular damage caused by amyloid PT deposits, partic. in haemorrhaging and Alzheimer's disease
 PS Example 1; Fig 1; 52pp; English.
 CC To investigate the effects of beta-amyloid peptide (BAP) on tissue plasminogen activator (t-PA) 3 synthetic peptides were used. One peptide contained 42 amino acids and corresp. to the full length BAP (R95248). The other 2 peptides (R95249 and 50) contained the 28 N-terminal residues of the BAP found in Alzheimer's disease and hereditary cerebral haemorrhage with amyloidosis-Dutch type (CHWA-D), respectively. In an assay to determine the effect of the peptides on t-PA activation, each peptide (R95248, 49 and 50) CC gave 1st order rate constant of activation (k_{app}) values of 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null CC and fibrinogen controls. The results demonstrate that the BAP are CC able to stimulate t-PA activity in vitro, which is significant in CC that it provides a means for investigating and controlling the CC pathogenesis of Alzheimer's disease, CHWA-D and cerebral amyloid CC angiopathy related cerebral haemorrhage.
 SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 9
 W01414
 ID W01414 standard; Protein; 28 AA.
 AC W01414;
 DT 20-JAN-1997 (first entry)
 DE Beta/A4-amyloid peptide residues 1-28 Dutch.
 KW Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;

KW control: cerebral amyloid angiopathy; cerebral; haemorrhage;

KW hemorrhage.

OS Homo sapiens.

FH Key Location/Qualifiers

FT misc_difference 22

FT /note= "wild type Glu substd. with Gln"

PN WO9615799-A1.

PD 30-MAY-1996.

PF 22-NOV-1995; US-347144.

PR (RUTF) UNIV RUTGERS STATE NEW JERSEY.

PA Anderson S;

PI WPI: 96-268332/27.

PT Use of agents which bind beta-amyloid peptide - for diagnosis,

PT prevention and treatment of vascular damage caused by amyloid

PT deposits, partic. in haemorrhaging and Alzheimer's disease

PS Example 1; Fig 1; 52pp; English.

CC To investigate the effects of beta-amyloid peptide (BAP) on

CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.

CC One peptide contained 42 amino acids and corresp. to the full

CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained

CC the 28 N-terminal residues of the BAP found in Alzheimer's disease

CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type

CC (HCHWA-D), respectively. In an assay to determine the effect of

CC the peptides on t-PA activation, each peptide (R95248, 49 and 50)

CC gave 1st order rate constant of activation (k(app)) values of

CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null

CC and fibrinogen controls. The results demonstrate that the BAP are

CC able to stimulate t-PA activity in vitro, which is significant in

CC that it provides a means for investigating and controlling the

CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid

CC angiopathy related cerebral haemorrhage.

CC Sequence 28 AA;

SQ

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 10

R64170

ID R64170 standard; peptide; 28 AA.

AC R64170;

DT 03-AUG-1995 (first entry)

DE A4-O(1-28) a partial beta amyloid peptide.

KW beta amyloid protein; mutant; variant; detection; amyloid deposition;

KW diagnosis; amyloidosis associated disease; Alzheimer's disease;

KW Down's syndrome; A4-O(1-28).

OS Synthetic.

PN WO9428412-A.

PD 08-DEC-1994.

PF 27-MAY-1994; US-05809.

PR 28-MAY-1993; US-065010.

PA (MIRI-) MIRIAM HOSPITAL.

PI Majocha RE, Marotta CA;

DR WPI: 95-023013/03.

PT Amyloid binding composition comprising labelled amyloid protein

PT and carrier - useful for in vivo imaging of amyloid deposits, for

PT diagnosing Alzheimer's disease and Down's Syndrome.

PS Example 1; Page 23; 58pp; English.

CC R64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the

CC 4.2 kb peptide deriv. from senile plaque cores of an AD (Alzheimer's

CC disease) brain, known as beta amyloid. A4-O has strong aggregation

CC properties, and binds to itself strongly. This peptide is used to obtain

CC and select beta amyloid proteins that can be used for in vivo imaging

CC of amyloid deposits and hence diagnosis of an amyloidosis-associated

CC disease, such as AD or Down's syndrome. R64165 shows the generic sequence

CC of the amyloid protein for generation of variants.

SQ Sequence 28 AA;

Query Match 100.0%; Score 92; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 11

R64172

ID R64172 standard; peptide; 28 AA.

AC R64172;

DT 03-AUG-1995 (first entry)

DE A4-B(1-28) a partial beta amyloid peptide.

KW beta amyloid protein; mutant; variant; detection; amyloid deposition;

KW diagnosis; amyloidosis associated disease; Alzheimer's disease;

KW Down's syndrome; A4-B(1-28).

OS Synthetic.

PN WO9428412-A.

PD 08-DEC-1994.

PF 27-MAY-1994; US-065010.

PR 28-MAY-1993; US-069010.

PA (MIRI-) MIRIAM HOSPITAL.

PI Majocha RE, Marotta CA;

DR WPI: 95-023013/03.

PT Amyloid binding composition comprising labelled amyloid protein

PT and carrier - useful for in vivo imaging of amyloid deposits, for

PT diagnosing Alzheimer's disease and Down's Syndrome.

PS Example 3; Page 23; 58pp; English.

CC R64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of the

CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the

CC 28 amino acids are different from the A4-O(1-28) peptide shown in R64170.

CC A4-O has strong aggregation properties, and binds to itself strongly. It

CC is used to obtain and select beta amyloid proteins that can be used for

CC in vivo imaging of amyloid deposits and hence diagnosis of an

CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165

CC shows the generic sequence of the amyloid protein for generation of

CC variants. 28 AA;

SQ Sequence 28 AA;

RESULT 12

W81467

ID W81467 standard; peptide; 28 AA.

AC W81467;

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).

KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;

KW research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 605090.

PR 29-FEB-1996; US-605090.

PA (KENT) UNIV KENTUCKY RES FOUND.

PI Aksenov M, Butterfield DA, Carney JM, Hensley K;

DR WPI: 99-034120/03.

PT Process for treating synthetic amyloid beta peptides - by organic

PT solvent treatment, useful for studying neurotoxicity

PT Claim 5; Columns 9-10; 14pp; English.

CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Query Match 100.0%; Score 92; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 13

ID W81468 standard; peptide; 30 AA.
AC W81468;
DT 28-JAN-1999 (first entry)
DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
OS Synthetic.
PN US5840838-A.
PD 24-NOV-1998.
PF 29-FEB-1996; 609090.
PR 29-FEB-1996; US-609090.
PA (KENT) UNIV KENTUCKY RES FOUND.
PI Aksekov M, Butterfield DA, Carney JM, Hensley K;
DR WPI; 99-034120/03.
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity
PS Claim 5; Columns 9-10; 14pp; English.
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Query Match 100.0%; Score 92; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14

W08359 standard; peptide; 33 AA.
ID W08359;
AC W08359;
DT 05-SEP-1997 (first entry)
DE Beta-secretase substrate #1.

KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
OS Synthetic.
PN W09640885-A2.
PD 19-DEC-1996.
PF 07-JUN-1996; U09985.
PR 07-JUN-1995; US-485152.
PR 07-JUN-1995; US-480498.
PR 07-JUN-1995; US-480498.
PA (ATHE-) ATHENA NEUROSCIENCES INC.
PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
PI McConlogue LC, Sinha S, Tan H;
DR WPI; 97-052304/05.
PT Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease
PT Alzheimer's disease
PS Disclosure; Page 44; 92pp; English.
CC W08359-W08362 represent substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP.
CC Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease.
CC Sequence 33 AA;
SQ

Query Match 100.0%; Score 92; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15

W81469
ID W81469 standard; peptide; 33 AA.
AC W81469;
DT 28-JAN-1999 (first entry)
DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).
KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
KW research; neurotoxicity; free-radical; glutamine synthetase.
OS Synthetic.
PN US5840838-A.
PD 24-NOV-1998.
PF 29-FEB-1996; 609090.
PR 29-FEB-1996; US-609090.
PA (KENT) UNIV KENTUCKY RES FOUND.
PI Aksekov M, Butterfield DA, Carney JM, Hensley K;
DR WPI; 99-034120/03.
PT Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity
PS Claim 5; Columns 9-10; 14pp; English.
CC Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide - enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical

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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:01 ; Search time 14.59 Seconds
(without alignments)
16.811 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92
Sequence: 1 DAEFRHDSGYEVHQQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	16	1	US-08-302-808-10
2	92	100.0	16	2	US-08-986-948-10
3	92	100.0	21	2	US-08-659-984A-18
4	92	100.0	27	1	US-08-141-324-11
5	92	100.0	27	1	US-08-141-324-12
6	92	100.0	27	1	US-08-541-902-11
7	92	100.0	27	1	US-08-541-902-12
8	92	100.0	28	1	US-08-346-849-4
9	92	100.0	28	1	US-08-302-808-7
10	92	100.0	28	2	US-08-609-090-2
11	92	100.0	28	2	US-08-986-948-7
12	92	100.0	28	2	US-08-293-284A-4
13	92	100.0	28	2	US-08-461-216-2
14	92	100.0	30	2	US-08-609-090-3
15	92	100.0	33	2	US-08-609-090-4
16	92	100.0	33	2	US-08-659-984A-16
17	92	100.0	35	1	US-08-304-585-6
18	92	100.0	35	2	US-08-612-785B-15
19	92	100.0	35	2	US-08-612-785B-38
20	92	100.0	36	2	US-08-609-090-6
21	92	100.0	38	1	US-08-302-808-1
22	92	100.0	38	2	US-07-737-371E-68
23	92	100.0	38	2	US-08-986-948-1
24	92	100.0	39	1	US-08-302-808-2
25	92	100.0	39	2	US-08-609-090-7
26	92	100.0	39	2	US-08-682-245A-1
27	92	100.0	39	2	US-08-986-948-2
28	92	100.0	40	1	US-07-744-767A-1

29 92 100.0 40 1 US-08-235-400-2 Sequence 2, Appli
30 92 100.0 40 1 US-08-476-464A-2 Sequence 2, Appli
31 92 100.0 40 1 US-08-304-585-1 Sequence 1, Appli
32 92 100.0 40 1 US-08-304-585-8 Sequence 8, Appli
33 92 100.0 40 1 US-08-302-808-3 Sequence 3, Appli
34 92 100.0 40 2 US-08-433-734-1 Sequence 1, Appli
35 92 100.0 40 2 US-08-609-090-8 Sequence 69, Appli
36 92 100.0 40 2 US-07-737-371E-69 Sequence 2, Appli
37 92 100.0 40 2 US-08-682-245A-2 Sequence 3, Appli
38 92 100.0 40 2 US-08-986-948-3 Sequence 1, Appli
39 92 100.0 40 4 US-08-461-216-1 Sequence 1, Appli
40 92 100.0 40 4 PCT-US92-06700-1 Sequence 1, Appli
41 92 100.0 41 1 US-07-819-361-1 Sequence 4, Appli
42 92 100.0 41 1 US-08-302-808-4 Sequence 3, Appli
43 92 100.0 41 2 US-08-682-245A-3 Sequence 4, Appli
44 92 100.0 41 2 US-08-986-948-4 Sequence 2, Appli
45 92 100.0 42 1 US-07-744-767A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-302-808-10
; Sequence 10, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

Wed Sep 13 08:11:39 2000

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
US-08-302-808-10

Query Match 100.0%; Score 92; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2
US-08-986-948-10
; Sequence 10, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhiro
; APPLICANT: ODAKA, Asano
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
US-08-986-948-10

Query Match 100.0%; Score 92; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.1e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
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Db 1 DAEFRHDSGYEVHHQK 16

RESULT 3
US-08-659-984A-18
; Sequence 18, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-659-984A-18

Query Match 100.0%; Score 92; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
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Db 6 DAEFRHDSGYEVHHQK 21

RESULT 4


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US-08-141-324-11
; Sequence 11, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Feiber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-141-324-11

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 5
US-08-141-324-12
; Sequence 12, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
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STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Feiber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-141-324-12

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 6
US-08-541-902-11
; Sequence 11, Application US/08541902
; Patent No. 5707620
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,902
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,324
; FILING DATE: 21-OCT-1993
; ATTORNEY/AGENT INFORMATION:
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us-09-155-076-2_1.rai

Wed Sep 13 08:11:39 2000

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; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 44-93
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-499-8080
; TELEFAX: 303-499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-541-902-11

Query Match 100.0%; Score 92; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 9 DAEFRHDSGYEVHHQK 24

RESULT 8
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: peptide
; MOLECULE TYPE: peptide
; US-08-346-849-4

Query Match 100.0%; Score 92; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9
US-08-302-808-7
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; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-302-808-7

Query Match 100.0%; Score 92; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | | | |
DB 1 DAEFRHDSGYEVHHQK 16

RESULT 10
US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth

; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-2

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Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
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DB 1 DAEFRHDSGYEVHHQK 16

RESULT 11
US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single

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; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; TOPOLOGY: linear
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; DESCRIPTION: {SYMBOL 98 \f "Symbol"}\A4(1-28);
; DESCRIPTION: page 83, line 31
US-08-461-216-2
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Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14
US-08-609-090-3
; Sequence 3, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-3
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; Sequence 4, Application US/08609090
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; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
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US-08-609-090-4
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About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 CompuGen Ltd.

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gb_pat:AA9528	+	92.00	296.89	1.9e-08	85	AA9528 Sequence 10 from Patent W
gb_pat:AG9920	+	92.00	291.45	3.9e-08	156	AG9920 Sequence 15 from Patent W
gb_om:SSAPPMR	+	92.00	290.42	4.4e-08	175	S56127 S.scrofa mrna for amyloid
gb_om:UAMPPMR	+	92.00	290.42	4.4e-08	175	S56127 S.scrofa mrna for amyloid
gb_om:CFAPPMR	+	92.00	290.37	4.5e-08	176	S56128 U.maritimus mrna for amyloid
gb_om:ORAPPMR	+	92.00	290.37	4.5e-08	176	S56125 C.familiaris mrna for amyloid
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gb_pat:AZ72184	+	92.00	284.12	9.9e-08	354	AZ7182 Sequence 8 from Patent W
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gb_pat:IO9368	+	92.00	271.06	5.3e-07	1521	AR003651 Sequence 3 from Patent W
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Wed Sep 13 08:11:40 2000

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seq_documentation_block: 156 bp DNA PAT 07-MAY-1999
LOCUS A69920
DEFINITION Sequence 15 from Patent WO9807850.
ACCESSION A69920
VERSION A69920.1 GI:4774427
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 156)
AUTHORS
Predde, E.R. and Bergmann, J.E.
TITLE
AGENTS FOR PRE-SYMPTOMATIC DETECTION AND THERAPEUTIC TARGETING OF
ALZHEIMER'S DISEASE AND DOWN SYNDROME IN HUMANS
JOURNAL
PATENT: WO 9807850-A 26-FEB-1998;
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Percent Similarity: 100.000 Percent Identity: 100.000

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LOCUS SSAPPMR
DEFINITION S.scrofa mRNA for amyloid precursor protein.
ACCESSION X56127
VERSION X56127.1 GI:1895
KEYWORDS
amyloid polypeptide.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 175)
AUTHORS
Johnstone, E.M.
TITLE
Direct Submission
JOURNAL
Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE
2 (bases 1 to 175)
AUTHORS
Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and
Little, S.P.
TITLE
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE
92017079
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LOCUS UNAPPMR
DEFINITION U.maritimus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56128
VERSION X56128.1 GI:2165
KEYWORDS
amyloid polypeptide.
SOURCE polar bear.
ORGANISM Thalarchos maritimus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Carnivora; Fissipedia; Ursidae; Ursidae; Thalarchos.
REFERENCE
1 (bases 1 to 175)
AUTHORS
Johnstone, E.M.
TITLE
Direct Submission
JOURNAL
Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY,
LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE
2 (bases 1 to 175)
AUTHORS
Johnstone, E.M., Chaney, M.O., Norris, F.H., Pascual, R. and
Little, S.P.
TITLE
Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis
JOURNAL
Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE
92017079
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Little,S.P.
Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis
JOURNAL
MEDLINE
FEATURES
92017079

Location/Qualifiers
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seq_name: gb_om:BTAPPMR

seq_documentation_block:
LOCUS BTAPPMR 177 bp mRNA 14-JUL-1992
DEFINITION B.taurus mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56124
VERSION X56124.1 GI:82
KEYWORDS amyloid polypeptide.
SOURCE Bos taurus
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 177)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES Location/Qualifiers
1. 177
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="brain"
<1. >177
/codon_start=1
/product="amyloid precursor protein"
/protein_id="CAA39589.1"
/db_xref="GI:83"
/translation="ISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGG

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ...

Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

seq_name: gb_om:OVAPPMR

seq_documentation_block:
LOCUS OVAPPMR 178 bp mRNA 14-JUL-1992
DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56130
VERSION X56130.1 GI:1829
KEYWORDS amyloid polypeptide.
SOURCE Ovis sp.
ORGANISM Ovis sp.
REFERENCE 1 (bases 1 to 178)
AUTHORS Johnstone,E.M.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE 2 (bases 1 to 178)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES Location/Qualifiers
1. 178
/organism="Ovis sp."
/db_xref="taxon:9939"
/tissue_type="heart"
<1. >178
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/product="amyloid precursor protein"
/protein_id="CAA39595.1"
/db_xref="GI:1830"
/db_xref="SWISS-PROT:Q28757"
/translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ...

Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

BASE COUNT 49 a 30 c 49 g 49 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x BTAPPMR ..

Align seg 1/1 to: BTAPPMR from: 1 to: 177

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
19 GATGCAGAAATTCGACATGACTCAGGATATGAAGTCCATCATCAAAAA 66

seq_name: gb_om:OVAPPMR

seq_documentation_block:
LOCUS OVAPPMR 178 bp mRNA 14-JUL-1992
DEFINITION Ovis sp. mRNA for amyloid precursor protein (APP) (partial).
ACCESSION X56130
VERSION X56130.1 GI:1829
KEYWORDS amyloid polypeptide.
SOURCE Ovis sp.
ORGANISM Ovis sp.
REFERENCE 1 (bases 1 to 178)
AUTHORS Johnstone,E.M.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1990) E.M. Johnstone, ELI LILLY AND COMPANY, LILLY CORPORATE CENTER 0424, INDIANAPOLIS IN 46285, USA
REFERENCE 2 (bases 1 to 178)
AUTHORS Johnstone,E.M., Chaney,M.O., Norris,F.H., Pascual,R. and Little,S.P.
TITLE Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis
JOURNAL Brain Res. Mol. Brain Res. 10 (4), 299-305 (1991)
MEDLINE 92017079
FEATURES Location/Qualifiers
1. 178
/organism="Ovis sp."
/db_xref="taxon:9939"
/tissue_type="heart"
<1. >178
/codon_start=3
/product="amyloid precursor protein"
/protein_id="CAA39595.1"
/db_xref="GI:1830"
/db_xref="SWISS-PROT:Q28757"
/translation="SEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGV

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x OVAPPMR ...

Align seg 1/1 to: OVAPPMR from: 1 to: 178

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16

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|||||
18 GATGAGAATTCGACATGATCCGGATATGAAGTTCATCATCAAAA 65
seq_name: gb_pr1:HUMAPRA41

seq_documentation_block:
LOCUS HUMAPRA41 189 bp DNA PRI 31-OCT-1994
DEFINITION Human amyloid protein gene, exon X.
ACCESSION M29269
VERSION M29269.1 GI:178862
KEYWORDS amyloid protein.
SEGMENT 1 of 2
SOURCE Human DNA (library of T.Maniatis), clone lambda-41.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 189)
AUTHORS Johnstone,E.M., Chaney,M.O., Moore,R.E., Ward,K.E., Norris,F.H. and
Little,S.P.
TITLE Alzheimer's disease amyloid peptide is encoded by two exons and
shows similarity to soybean trypsin inhibitor
JOURNAL Biochem. Biophys. Res. Commun. 163 (3), 1248-1255 (1989)
MEDLINE 89392030
FEATURES
source
Location/Qualifiers
1..189
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21q21.2"
<1..42
/gene="APP"
/note="intron X-1; G00-119-692"
43..143
/gene="APP"
/note="exon X; G00-119-692"
/sequence="exon X; G00-119-692"
59 a 32 c 38 g 60 t
BASE COUNT 59 a 32 c 38 g 60 t
ORIGIN 73 bp upstream of BglII site; chromosome 21q21.2.

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x HUMAPRA41 ..
Align seg 1/1 to: HUMAPRA41 from: 1 to: 189

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
93 GATGAGAATTCGACATGACTGAGTATGAAGTTCATCATCAAAA 140

seq_name: gb_pr1:HUMAMYB1

seq_documentation_block:
LOCUS HUMAMYB1 242 bp DNA PRI 31-OCT-1994
DEFINITION Human amyloid-beta protein DNA, exon 14.
ACCESSION M37895
VERSION M37895.1 GI:178617
KEYWORDS amyloid-beta protein.
SEGMENT 1 of 2
SOURCE Human (Dutch patient with hereditary cerebral hemorrhage with
amyloidosis) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 242)
AUTHORS Levy,E., Carman,M.D., Fernandez-Madrid,I.J., Power,M.D.,
Lieberburg,I., van Duinen,S.G., Bots,G.T., Luyendijk,W. and
Frangione,B.
TITLE Mutation of the Alzheimer's disease amyloid gene in hereditary
cerebral hemorrhage, Dutch type
JOURNAL Science 248 (4959), 1124-1126 (1990)

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MEDLINE 90260663 Location/Qualifiers
FEATURES source
1..242
/organism="Homo sapiens"
/isolate="hereditary cerebral hemorrhage with amyloidosis
of Dutch type patient"
/db_xref="taxon:9606"
/map="21q21.2"
<1..103
/organism="Homo sapiens"
/note="G00-119-692"
/number=1
/sequence="APP"
205..242
/gene="APP"
BASE COUNT 75 a 35 c 52 g 80 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x HUMAMYB1 ..
Align seg 1/1 to: HUMAMYB1 from: 1 to: 242

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
154 GATGAGAATTCGACATGACTGAGTATGAAGTTCATCATCAAAA 201

seq_name: gb_pr2:S60721

seq_documentation_block:
LOCUS S60721 246 bp mRNA PRI 23-JUL-1993
DEFINITION beta-amyloid peptide precursor (clone 1) [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S60721
VERSION S60721.1 GI:299644
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman,R.B., Rosenczwaig,R. and Miller,D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 129915] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.
Location/Qualifiers
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/partial
/gene="beta-amyloid peptide precursor, beta APP"
1..246
/partial
/gene="beta-amyloid peptide precursor, beta APP"
/note="This sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(44[K->N],73[W->Y],76[I->N]); beta APP"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26263.1"
/db_xref="GI:299645"

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/translation="GSLTNKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGAIIGLMVGGVVIAIVITLVLMLKKQWTSIHGGVVE"

BASE COUNT 72 a 40 c 69 g 65 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x S60721 ..

Align seg 1/1 to: S60721 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61380

seq_documentation_block: 246 bp mRNA PRI 23-JUL-1993
LOCUS S61380
DEFINITION beta-amyloid peptide precursor (clone 2) [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61380
VERSION S61380
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman, R.B., Rosenczwaig, R. and Miller, D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132963] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
source
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene
1..246
/partial
/gene="beta-amyloid peptide precursor, beta App"
CDS
1..246
/partial

/gene="beta-amyloid peptide precursor, beta App"
/note="This sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(44[K->N],73[W->Y],76[I->N]); beta App"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26264.1"
/db_xref="GI:299647"
/translation="GSLTNKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGAIIGLMVGGVVIAIVITLVLMLKKQWTSIHGGVVE"

BASE COUNT 73 a 40 c 69 g 64 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x S61380 ..

Align seg 1/1 to: S61380 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

seq_name: gb_pr2:S61383

seq_documentation_block: 246 bp mRNA PRI 23-JUL-1993
LOCUS S61383
DEFINITION beta-amyloid peptide precursor (clone 3) [human, mRNA Partial
Mutant, 246 nt].
ACCESSION S61383
VERSION S61383
KEYWORDS
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 246)
AUTHORS Denman, R.B., Rosenczwaig, R. and Miller, D.L.
TITLE A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor
JOURNAL Biochem. Biophys. Res. Commun. 192 (1), 96-103 (1993)
MEDLINE 93236601
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 132966] from the original journal article.
This sequence comes from Fig. 1.
Map location: 21.

FEATURES
Location/Qualifiers
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene
1..246
/partial
/gene="beta-amyloid peptide precursor, beta App"
CDS
1..246
/partial
/gene="beta-amyloid peptide precursor, beta App"
/note="This sequence comes from Fig. 1; Protein sequence
is in conflict with the conceptual translation;
mismatches(698[K->N],727[W->Y],730[I->N]); beta App"
/codon_start=1
/product="beta-amyloid peptide precursor"
/protein_id="AAB26265.1"
/db_xref="GI:299649"
/translation="GSLTNKTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSK
KGAIIGLMVGGVVIAIVITLVLMLKKQWTSIHGGVVE"

BASE COUNT 72 a 40 c 71 g 63 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x S61383 ..

Align seg 1/1 to: S61383 from: 1 to: 246

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
52 GATGCAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 99

OM of: US-09-155-076-2 to: N_Geneseq_36.* out_format : pfs

Date: Sep 13, 2000 2:58 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODE=frame+p2n.model -DEV=xlip
-O=/sgn2_1/USPFO_spool/US09155076/runat_29082000_092505_15779/app_query.fasta_1.144
-DB=N_Geneseq_36 -QFMT=fastp -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DCLIGN=200 -THR_SCORE=pct
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-NORM-ext -MINLEN=0 -MAXLEN=1000000 -USER=US09155076_RCGN1_1_75
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: N_Geneseq_36.*

Database sequences: 311585

Database length: 125096042

Search time (sec): 75.680000

score_list:

Sequence	Strd	Orig	ZScore	Escore	Len	Documentation
N_Geneseq_36:T38687	+	92.00	295.99	6.9e-09	58	Mouse amyloid precursor protein
N_Geneseq_36:T14516	+	92.00	292.49	1.1e-08	85	Beta-amyloid4 peptide coding sequence
N_Geneseq_36:N92266	+	92.00	285.75	2.6e-08	177	Region of pre-APP coding sequence
N_Geneseq_36:Q77922	+	92.00	285.15	2.8e-08	189	CDNA encoding the APP leader sequence
N_Geneseq_36:V23754	+	92.00	282.15	4.1e-08	262	Alzasi coding sequence. Nucleic
N_Geneseq_36:Q88696	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88697	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q88698	+	92.00	281.00	4.7e-08	297	Beta-amyloid precursor protein
N_Geneseq_36:Q10017	+	92.00	280.91	4.8e-08	300	Sequence encoding beta-amyloid
N_Geneseq_36:Q42655	+	92.00	280.91	4.8e-08	300	Full-length beta-amyloid protein
N_Geneseq_36:Q88699	+	92.00	280.64	5.0e-08	309	Beta-amyloid precursor protein
N_Geneseq_36:Q88700	+	92.00	280.64	5.0e-08	309	Beta-amyloid precursor protein
N_Geneseq_36:T18082	+	92.00	279.87	5.5e-08	336	Familial Alzheimer's disease AP
N_Geneseq_36:V20377	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20380	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20381	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20378	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V20379	+	92.00	279.39	5.8e-08	354	DNA for APP C-terminal fragment
N_Geneseq_36:V07188	+	92.00	279.39	5.8e-08	354	Flag-amyloid protein precursor
N_Geneseq_36:X08982	+	92.00	279.39	5.8e-08	354	Amlyoid precursor protein (APP)
N_Geneseq_36:V20382	+	92.00	279.24	5.9e-08	360	DNA for APP C-terminal fragment
N_Geneseq_36:N80605	+	92.00	276.48	8.5e-08	486	Lambda SM2 encoding first 18 am
N_Geneseq_36:Q10015	+	92.00	276.48	8.5e-08	486	Genomic clone including beta-am
N_Geneseq_36:Q42662	+	92.00	275.86	9.2e-08	520	Human beta amyloid fusion prote
N_Geneseq_36:Q82910	+	92.00	275.86	9.2e-08	520	Alzaz coding sequence. Nucleic
N_Geneseq_36:V23753	+	92.00	266.11	3.2e-07	1504	CDNA sequence of clone amy 37
N_Geneseq_36:N90497	+	92.00	266.01	3.2e-07	1521	Maltose binding protein-APP (S
N_Geneseq_36:N90397	+	92.00	265.77	3.3e-07	1562	CDNA sequence of amy 37 clone.
N_Geneseq_36:Q54257	+	92.00	264.88	3.7e-07	1721	APP-REP 751 amyloid precursor
N_Geneseq_36:Q69003	+	92.00	263.11	4.7e-07	2085	Mouse amyloid precursor protei
N_Geneseq_36:Q27801	+	92.00	263.10	4.7e-07	2088	APP695. Polynucleotide probe c
N_Geneseq_36:N80604	+	92.00	262.39	5.2e-07	2256	Lambda APCP16844, amino acids 1
N_Geneseq_36:Q10014	+	92.00	262.39	5.2e-07	2256	Clone lambda APCP16814 of beta
N_Geneseq_36:Q20532	+	92.00	262.39	5.2e-07	2256	Sequence of clone lambdaAPC16
N_Geneseq_36:Q42661	+	92.00	262.39	5.2e-07	2256	Lambda clone APCP16814 encodes
N_Geneseq_36:Q27802	+	92.00	262.35	5.2e-07	2265	APP751. Polynucleotide probe c
N_Geneseq_36:X08983	+	92.00	262.35	5.2e-07	2265	Amyloid precursor protein (APP
N_Geneseq_36:V10322	+	92.00	262.17	5.3e-07	2310	Human APP770 cDNA. Identifying
N_Geneseq_36:Q48860	+	92.00	262.16	5.3e-07	2313	Mutated APP770 exon 17 DNA. Ne
N_Geneseq_36:Q74700	+	92.00	262.16	5.3e-07	2313	CDNA of APP 770 gene contg. mu

N_Geneseq_36:N91050 + 92.00 259.93 7.1e-07 2949 ! Sequence encoding novel amy
N_Geneseq_36:Q05086 + 92.00 259.93 7.1e-07 2949 ! Sequence encodes NAP-2 gene
N_Geneseq_36:N91049 + 92.00 259.76 7.2e-07 3006 ! Sequence encoding novel amy
N_Geneseq_36:Q05085 + 92.00 259.76 7.2e-07 3006 ! Sequence encodes NAP gene a

seq_name: N_Geneseq_36:T38687

seq_documentation_block:

ID T38687 standard; DNA; 58 BP.

AC T38687;

DT 21-JUL-1997 (first entry)

DE Mouse amyloid precursor protein exon 16 primer ST61.

KW Exon 16; murine; mouse; amyloid; precursor; protein; APP;

KW humanisation; homozygous; heterozygous; human; Abeta; Swedish;

KW familial; Alzheimer's; disease; FAD; mutation; tool; model;

KW elucidation; pathology; symptomatology; screen; inhibition;

KW transgenic; polymerase chain reaction; primer; PCR;

KW amplification; ss.

OS Synthetic.

PN N09634097-AL.

PD 31-OCT-1996.

PF 26-APR-1996; U05824.

PR 26-APR-1996; US-429207.

PR 23-APR-1996; US-636876.

PA (CEPH-) CEPHALON INC.

PI Hoffman EK, Reaume AG, Scott RW, Siman R, Trusko SP;

DR WPI; 96-497629/49.

PT Transgenic mice with humanised amyloid precursor protein gene -

PT having at least 1 Swedish FAD mutation, useful as tools or models to

PT elucidate role of human A-beta in Alzheimer's disease

PS Example 1; Page 75; 123pp; English.

CC The present sequence is a primer for the PCR amplification of exon

CC 16 of the mouse amyloid precursor protein (APP) gene, into which 6

CC humanising base pair changes was introduced. The exon was then used

CC in the preparation of mice homozygous or heterozygous for a

CC targeted APP encoding gene, comprising a human Abeta peptide

CC encoding sequence in place of the endogenous murine sequence, and

CC at least 1 Swedish Familial Alzheimer's Disease (FAD) mutation. The

CC mice can be used as tools, or models to elucidate the role of human

CC Abeta in AD pathology and symptomatology. They can also be used to

CC screen chemical compounds for the ability to inhibit in vivo

CC processing of APP, to yield the human Abeta peptide by

CC administering the chemical compounds to a mouse and measuring the

CC relative amounts of amyloidogenic and nonamyloidogenic processing

CC of APP in a sample from the mouse at an appropriate interval after

CC administration of the chemical compounds.

SQ Sequence 58 BP; 23 A; 11 C; 13 T;

alignment_scores:

Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x T38687

Align seg 1/1 to: T38687 from: 1 to: 58

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
8 GATGCAGAAATTCAGACATGATTCAGGATATGAGTCCACCATCAAAA 55

seq_name: N_Geneseq_36:T14516

seq_documentation_block:

ID T14516 standard; DNA; 85 BP.

AC T14516;

DT 30-OCT-1996 (first entry)

DE Beta-amyloid4 peptide coding sequence.

DE Unfolded-protein-response element; UPR; BIP; expression cassette; p53;

KW reporter element; protein misfolding; prion; beta-amyloid peptide; plant;

KW host cell; animal; insect cell; fungal cell; saccharomyces cerevisiae;

58 GATCGAGATTCCGACATGACTCAGGATATGAACTTCATCATCAAAAA 105

seq_name: N_Geneseq_36.V23754

seq_documentation_block:

ID V23754 standard; DNA; 262 BP.

AC V23754;

DT 18-AUG-1998 (first entry)

DE Alzasl coding sequence.

KW Dsas; DSASP; alzsl; Down's syndrome; diagnosis; therapy; human;

KW Alzheimer's disease; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 50..205

FT /*tag= a

FT /product= ALZASpl

FT /note= "specifically claimed fragment"

FN WO9807850-A2.

PD 26-FEB-1998.

PF 22-AUG-1997; E04599.

PR 22-AUG-1996; CA-183901.

PA (BERG/) BERGMANN J E.

PA (PRED/) FREDDIE E R.

PI Bergmann JE, Freddie ER;

DR WPI: 98-169155/15.

DR P-PSDB: W53984.

PT Nucleic acid molecules dsas, and alzsl - used for detecting and

PT treating Down's syndrome and Alzheimer's disease

PS Claim 13; Fig 11; 96pp; English.

CC This sequence represents the human alzsl nucleic acid. The dsas

CC and alzsl DNA sequences are the nucleic acids of the invention. Reagents

CC specifically for DSASP can be used for the diagnosis of Down's syndrome

CC in humans and especially in pregnant women. Molecules that inhibit the

CC activity of the promoters (PDS1, PDS2, and PDS4) for dsas can be

CC used for treating Down's syndrome. The reagent capable of detecting

CC alzsl can be used for detecting Alzheimer's disease, especially in the

CC pre-symptomatic stage. Substances that inhibit the promoters for alzsl

CC can be used in treating Alzheimer's disease.

SQ Sequence 262 BP; 96 A; 43 C; 52 G; 71 T;

alignment_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

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Align seg 1/1 to: V23754 from: 1 to: 262

1 ASPALAGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

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53 GATCGAGATTCCGACATGACTCAGGATATGAACTTCATCATCAAAAA 100

seq_name: N_Geneseq_36.Q88696

seq_documentation_block:

ID Q88696 standard; cDNA to mRNA; 297 BP.

AC Q88696;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide gene.

KW Human; beta-amyloid precursor protein; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH) HOECHST JAPAN LTD.

PA (FARH) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB: R74694.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta-amyloid precursor protein in a gene construct designed for over-expression in various cell types

PS Claim 2; Page 11; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein (APP) C-terminal peptide. The DNA may be transferred along with an

CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells of

CC a non-human mammal, and the resulting transgenic animal may be used

CC as a model for Alzheimer disease (AD). The animal model exhibits

CC symptoms similar to AD, producing large quantities of APP C-terminal

CC peptide, death of neuron cells in pyramidal cells at cerebral

CC amyloid regions, increases in glial cells and deposition of

CC abnormally phosphorylated tau protein. The animal model may be

CC used to develop new therapies for AD, including gene therapy

CC strategies.

SQ Sequence 297 BP; 86 A; 64 C; 78 G; 69 T;

alignment_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q88696 ..

Align seg 1/1 to: Q88696 from: 1 to: 297

1 ASPALAGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||

1 GATCGAGATTCCGACATGACTCAGGATATGAACTTCATCATCAAAAA 48

seq_name: N_Geneseq_36.Q88697

seq_documentation_block:

ID Q88697 standard; cDNA to mRNA; 297 BP.

AC Q88697;

DT 11-NOV-1995 (first entry)

DE Beta-amyloid precursor protein C-terminal peptide mutant gene.

KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;

KW gene transfer; transgenic animal; Alzheimer disease model;

KW gene therapy; ss.

OS Homo sapiens.

PN EP-653154-A.

PD 17-MAY-1995.

PF 07-NOV-1994; 117512.

PR 12-NOV-1993; JP-306026.

PA (FARH) HOECHST JAPAN LTD.

PA (FARH) HOECHST JAPAN KK.

PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;

DR WPI: 95-180492/24.

DR P-PSDB: R74695.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding part of beta-amyloid precursor protein in a gene construct designed for over-expression in various cell types

PS Claim 2; Page 12-13; 32pp; English.

CC The sequence encodes a human brain beta-amyloid precursor protein

CC (APP) mutant C-terminal peptide, and differs from Q88696 by a Glu

CC to Gln conversion at codon-22. The DNA may be transferred along

CC with an APP signal peptide gene (e.g. Q88695) into somatic and germ

CC cells of a non-human mammal, and the resulting transgenic animal may

CC be used as a model for Alzheimer disease (AD). The animal model

CC exhibits symptoms similar to AD, producing large quantities of APP

CC C-terminal peptide, death of neuron cells in pyramidal cells at

CC cerebral amyloid regions, increases in glial cells and deposition

CC of abnormally phosphorylated tau protein. The animal model may

CC be used to develop new therapies for AD, including gene therapy

CC strategies.

SQ Sequence 297 BP; 86 A; 65 C; 77 G; 69 T;

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alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
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  Align seg 1/1 to: Q88697 from: 1 to: 297

  1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  1 GATCGAGAAATCCGACATGACTCAGGATATGAGATTTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q88698

seq_documentation_block:
  ID Q88698 standard; cDNA to mRNA; 297 BP.
  AC Q88698; 1995 (first entry)
  DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
  KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
  KW gene transfer; transgenic animal; Alzheimer disease model;
  KW gene therapy; ss.
  OS Homo sapiens.
  PN EP-653154-A.
  PD 17-MAY-1995.
  PF 07-NOV-1994; 117512.
  PR 12-NOV-1993; JP-306026.
  PA (FARH ) HOECHST JAPAN LTD.
  PA (FARH ) HOECHST JAPAN KK.
  PI Kawabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
  DT WPI; 95-180492/24.
  DR P-PSDB; R74696.
  PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
  part of beta-amyloid precursor protein in a gene construct designed for
  over-expression in various cell types
  PS Claim 2; Page 13-14; 32pp; English.
  CC The sequence encodes a human brain beta-amyloid precursor protein
  (APP) mutant C-terminal peptide, and differs from Q88696 by
  conversion of Val to Ile at codon-46. The DNA may be transferred
  along with an APP signal peptide gene (e.g. Q88695) into somatic and
  germ cells of a non-human mammal, and the resulting transgenic animal
  may be used as a model for Alzheimer disease (AD). The animal model
  exhibits symptoms similar to AD, producing large quantities of APP
  C-terminal peptide, death of neuron cells in pyramidal cells at
  cerebral amyloid regions, increases in glial cells and deposition
  of abnormally phosphorylated tau protein. The animal model may
  be used to develop new therapies for AD, including gene therapy
  strategies.
  SQ Sequence 297 BP; 87 A; 64 C; 77 G; 69 T;

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x Q88698 ..
  Align seg 1/1 to: Q88698 from: 1 to: 297

  1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  1 GATCGAGAAATCCGACATGACTCAGGATATGAGATTTCATCATCAAAAA 48

seq_name: N_Geneseq_36:Q10017

seq_documentation_block:
  ID Q10017 standard; DNA; 300 BP.
  AC Q10017;
  DT 14-MAR-1991 (first entry)

```

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DE Sequence encoding beta-amyloid-related protein.
KW Alzheimer's disease; AD; acute pancreatitis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..300
FT /*tag= a
FT WO9014840-A.
FT 13-DEC-1990.
FT 04-JUN-1990; U03141.
FT 06-JUN-1989; US-361912.
FT 29-MAR-1990; US-502273.
FT (CALB-) CALIF BIOTECH INC.
FT Schilling JW, Ponte PA, Cordell B;
FT WPI; 91-006983/01.
FT R-PSDB; R10024.
FT DNA sequences, and protease inhibitors encoded by them and
FT antibodies - for diagnosis and treatment of alzhemlers disease
FT Disclosure; Fig 5; 96pp; English.
FT Sequence may be useful in prognosis and diagnosis of human
FT Alzheimer's disease (AD). Abs may be raised to the gene product, and
FT probes derived from the encoding sequence allowing diagnosis and
FT determination of genetic predisposition.
FT The gene product is a protease inhibitor and may also have utility
FT in treatment of acute pancreatitis.
SQ Sequence 300 BP; 87 A; 63 C; 80 G; 70 T;

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x Q10017 ..
  Align seg 1/1 to: Q10017 from: 1 to: 300

  1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
  |||||
  4 GATCGAGAAATCCGACATGACTCAGGATATGAGATTTCATCATCAAAAA 51

seq_name: N_Geneseq_36:Q42665

seq_documentation_block:
  ID Q42665 standard; cDNA; 300 BP.
  AC Q42665; 1993 (first entry)
  DE Full-length beta-amyloid protein coding region.
  KW Alzheimer's Disease; Amyloid Plaque Core Protein; APCP;
  KW neuritic plaque; ds.
  OS Homo sapiens.
  FH Key Location/Qualifiers
FT cds 1..300
FT /*tag= a
FT /product= beta-amyloid_protein
FT /note= "full-length coding sequence obtained by
FT combining overlapping clones SM2W3 and
FT SM2W4 (Q42664 and Q42663, respectively)"
FT misc_difference 160..162
FT /*tag= b
FT /codon= seq: AAC; aa: Lys
FT /note= "this codon is AAG in Q42664"
FT US5220013-A.
FT 15-JUN-1993.
FT 17-NOV-1986; 932193.
FT 17-NOV-1986; US-932193.
FT 31-DEC-1986; US-948376.
FT 30-JAN-1987; US-008810.
FT 18-AUG-1987; US-087002.
FT 30-NOV-1989; US-444118.
FT (SCIO-) SCIOS NOVA INC.
FT Cordell B, Ponte PA;
FT WPI; 93-205383/25.

```


DR P-PSDB: R37866.
 PT DNA sequence useful for detection of Alzheimer's disease - for
 PS encoding beta amyloid core protein
 CC Disclosure; Fig 5; 40pp; English.
 CC A clone was obtained from the genomic library described in Lawn et al.,
 CC Cell, 15:1157-1174 (1978) which included a 57 base pair segment which
 CC encodes amino acids 1-18 of the beta-amyloid protein. Immediately
 CC preceded by a Methionine. A HindIII/RsaI fragment derived from the
 CC genomic clone and containing the 57bp segment was used to isolate cDNA
 CC fragments from a library prepared from temporal and parietal cortical
 CC tissue from a normal human brain. Lambda clone SM2W3 (Q42664) contains
 CC a 5' region segment which has a 6bp overlap with the 3' end of clone
 CC SM2W4 (Q42663). The full-length beta-amyloid protein coding sequence
 CC (Q42665), including an initiator Met residue which is probably
 CC processed in vivo, was obtained by combining the sequences of the
 CC two overlapping clones.
 SQ Sequence 300 BP; 87 A; 65 C; 78 G; 70 T;

alignment_scores:
 Quality: 92.00 Length: 16
 Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q42665 ..

Align seg 1/1 to: Q42665 from: 1 to: 300

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 4 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 51

seq_name: N_Geneseq_36:Q88699

seq_documentation_block:

ID Q88699 standard; cDNA to mRNA; 309 BP.

AC Q88699;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide gene.
 KW Human; beta-amyloid precursor protein; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI: 95-180492/24.
 DR P-PSDB: R74697.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types

PS Claim 2; Page 15; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The DNA may be transferred along with an
 CC APP signal peptide gene (e.g. Q88695) into somatic and germ cells
 CC of a non-human mammal, and the resulting transgenic animal may be
 CC used as a model for Alzheimer disease (AD). The animal model
 CC exhibits symptoms similar to AD, producing large quantities of APP
 CC C-terminal peptide, death of neuron cells in pyramidal cells at
 CC cerebral amyloid regions, increases in glial cells and deposition
 CC of abnormally phosphorylated tau protein. The animal model may
 CC be used to develop new therapies for AD, including gene therapy
 CC strategies.

SQ Sequence 309 BP; 91 A; 64 C; 83 G; 71 T;

alignment_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q88699 ..

Align seg 1/1 to: Q88699 from: 1 to: 309

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq_name: N_Geneseq_36:Q88700

seq_documentation_block:

ID Q88700 standard; cDNA to mRNA; 309 BP.

AC Q88700;
 DT 11-NOV-1995 (first entry)
 DE Beta-amyloid precursor protein C-terminal peptide mutant gene.
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy; ss.
 OS Homo sapiens.
 PN EP-653154-A.
 PD 17-MAY-1995.
 PF 07-NOV-1994; 117512.
 PR 12-NOV-1993; JP-306026.
 PA (FARH) HOECHST JAPAN LTD.
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 DR WPI: 95-180492/24.
 DR P-PSDB: R74698.

PT Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types

PS Claim 2; Page 16-17; 32pp; English.
 CC The sequence encodes a human brain beta-amyloid precursor protein
 CC (APP) mutant C-terminal peptide, and differs from Q88699 by
 CC conversion of Lys to Asn at codon-3 and Met to Leu at codon-4. The
 CC DNA may be transferred along with an APP signal peptide gene (e.g.
 CC Q88695) into somatic and germ cells of a non-human mammal, and the
 CC resulting transgenic animal may be used as a model for Alzheimer
 CC disease (AD). The animal model exhibits symptoms similar to AD,
 CC producing large quantities of APP C-terminal peptide, death of
 CC neuron cells in pyramidal cells at cerebral amyloid regions,
 CC increases in glial cells and deposition of abnormally
 CC phosphorylated tau protein. The animal model may be used to develop
 CC new therapies for AD, including gene therapy strategies.

alignment_scores:

Quality: 92.00 Length: 16
 Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x Q88700 ..

Align seg 1/1 to: Q88700 from: 1 to: 309

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 13 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCATCAAAAA 60

seq_name: N_Geneseq_36:T18082

seq_documentation_block:

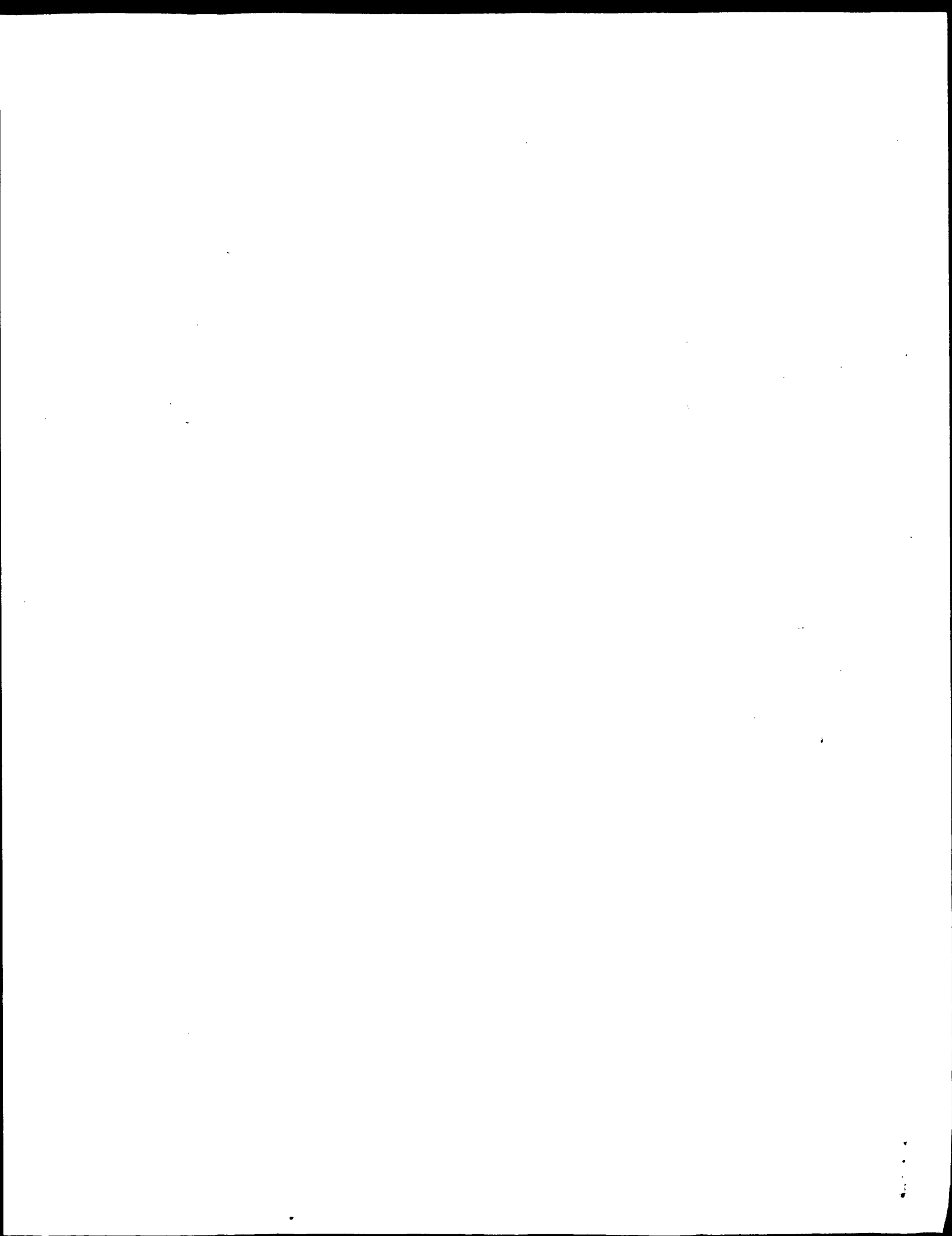
ID T18082 standard; DNA; 336 BP.

AC T18082;
 DT 10-OCT-1996 (first entry)
 DE Familial Alzheimer's disease APP isoform 751 gene fragment.
 KW APP; amyloid precursor protein; isoform 751; inherent; familial;

PS Claim 10: Page 11; 15pp; English.
 CC The present sequence encodes the human amyloid precursor protein
 CC (APP) C-terminal fragment (M4CT) mutant SP4ACT Thr43Ala/Val46Phe.
 CC The mutation results in a higher ratio of beta A4 1-42 to beta A4
 CC 1-40, useful in disease models to identify potential drugs for the
 CC treatment of Alzheimer's disease.
 SQ Sequence 354 BP; 91 A; 82 C; 98 G; 83 T;

alignment_scores:
 Quality: 92.00 Length: 16
 Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-2 x V20380 ..
 Align seg 1/1 to: V20380 from: 1 to: 354
 1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
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 58 GATGCAGANTCCGACATGACTCAGGATATGAGTTTCATCATCAAAAA 105



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 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

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/cgn2_6/ptodata/2/ina/5D.COMB.seq:US-08-422-333-22 +	92.00	285.70	2.0e-08	486	1
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 seq_documentation_block:
 ; Sequence 15, Application US/08636876
 ; Patent No. 5777194
 ; GENERAL INFORMATION:
 ; APPLICANT: Scott, Richard W.
 ; APPLICANT: Reame, Andrew G.
 ; APPLICANT: Trusko, Stephen P.
 ; APPLICANT: Siman, Robert
 ; TITLE OF INVENTION: GENE-TARGETED NON-HUMAN MAMMAL WITH
 ; TITLE OF INVENTION: HUMANIZED AB SEQUENCE AND SWEDISH FAD MUTATIONS
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street Suite 3100
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/636,876
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 02655/055001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 58 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-636-876-15
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 8 GATGCAGAAATTCAGACATGATTCAGATATGAGTCCACCATCAAAA 55
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 seq_documentation_block:
 ; Sequence 8, Application PC/TUS9404026
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Transgenic Animal Models for Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 12

Wed Sep 13 08:11:41 2000

us-09-155-076-2_1.rni

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower - 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-8402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04026
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, Ph.D., David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31188
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Human
ORGANISM: Human
PCT-US94-04026-8

alignment_scores:
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Ratio: 5.750 Gaps: 0
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seq_documentation_block:
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Patent No. 6037521
GENERAL INFORMATION:
APPLICANT: Sato, Masahiro
APPLICANT: Takashi, Kobayashi
APPLICANT: Tada, No. 6037521hiro
APPLICANT: Shoji, Mikio
APPLICANT: Kawarabayashi, Takeshi
TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,708A
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306026/93
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904135
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
STRAIN: human brain
FEATURE:
NAME/KEY: CDS
LOCATION: 1..297
OTHER INFORMATION: /note= "1. human beta-amyloid
precursor; 2. C-terminal peptide"
US-08-339-708A-3

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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seq_documentation_block:
Sequence 5, Application US/08339708A
Patent No. 6037521
GENERAL INFORMATION:
APPLICANT: Sato, Masahiro
APPLICANT: Takashi, Kobayashi
APPLICANT: Tada, No. 6037521hiro
APPLICANT: Shoji, Mikio
APPLICANT: Kawarabayashi, Takeshi
TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-5

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alignment_scores:
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  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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alignment_block:
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Align seg 1/1 to: US-08-339-708A-5 from: 1 to: 297
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seq_documentation_block:
; Sequence 7, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..297
; OTHER INFORMATION: /note= "1. human beta-amyloid
; OTHER INFORMATION: precursor; 2. C-terminal peptide"
; US-08-339-708A-7

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alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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alignment_block:
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seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:9:

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; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,708A
; FILING DATE: 14-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 306026/93
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, COLIN G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; STRAIN: human brain
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..309
; OTHER INFORMATION: /note= "1. human beta-amylloid precursor; 2. C-terminal peptide"
; US-08-339-708A-9

alignment_scores:
    Quality: 92.00      Length: 16
    Ratio: 5.750        Gaps: 0
    Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-339-708A-9 ..
Align seg 1/1 to: US-08-339-708A-9 from: 1 to: 309

seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-339-708A-11

seq_documentation_block:
; Sequence 11, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
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;; TITLE OF INVENTION: DISEASE
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICANT: Patent In Release #1.0, Version #1.30
;; APPLICATION NUMBER: US/08-339,708A
;; FILING DATE: 14-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 306026/93
;; FILING DATE: 12-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SANDERCOCK COLIN G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 026083/0159
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 309 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: homo sapiens
;; STRAIN: human brain
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..309
;; OTHER INFORMATION: /note= "1. human beta-amyloid
;; OTHER INFORMATION: precursor; 2. C-terminal peptide"
US-08-339-708A-11

alignment_scores:
  Quality: 92.00 Length: 16
  Ratio: 5.750 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
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Align seg 1/1 to: US-08-339-708A-11 from: 1 to: 309
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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13 GATGAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 60
seq_name: /cgn2_6/ptodata/2/1na/5c_comb.seq:US-08-729-345-2
seq_documentation_block:
; Sequence 2, Application US/08729345
; Patent No. 5849999
; GENERAL INFORMATION:
; APPLICANT: Neve, Rachael L.
; APPLICANT: Berger-Sweeney, Joanne
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL
; TITLE OF INVENTION: EXPRESSING FLAG-APP-C100 FUSION PROTEIN
; NUMBER OF SEQUENCES: 9
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;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: US
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/729,345
;; FILING DATE: 16-OCT-1996
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 04843/027001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-542-5070
;; TELEFAX: 617-542-8906
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 354 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 1..351
;; OTHER INFORMATION:
US-08-729-345-2

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  Ratio: 5.750 Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
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Align seg 1/1 to: US-08-729-345-2 from: 1 to: 354
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55 GATGAGATTCCGACATGACTCAGGATATGAAGTTCATCATCAAAA 102
seq_name: /cgn2_6/ptodata/2/1na/backfiles1.seq:5187153-3
seq_documentation_block:
; Patent No. 5187153
; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
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us-09-155-076-2_1.rni

Wed Sep 13 08:11:41 2000

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;
; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
; LENGTH: 486
5187153-3

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  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
240 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 287

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5220013-3

seq_documentation_block:
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.;CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
; LENGTH: 486
5220013-3

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
241 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 288

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5223482-3

seq_documentation_block:
; Patent No. 5223482
; APPLICANT: SCHILLING, JAMES W.;PONTE, PHYLLIS A.;CORDELL,
; BARBARA
; TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
; INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/361,912
; FILING DATE: 06-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO:3:
; LENGTH: 486
5223482-3

alignment_scores:
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  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  US-09-155-076-2 x 5223482-3 ..
  Align seg 1/1 to: 5223482-3 from: 1 to: 486

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241 GATGCGAATTCGACATGACTCAGGATATGAAGTTCATCAAAAA 288

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-268-348A-9

seq_documentation_block:
; Sequence 9, Application US/08268348A
; Patent No. 5750374
; GENERAL INFORMATION:
; APPLICANT: Dobeli, Heinz
; APPLICANT: Draeger, Nicholas
; APPLICANT: Trotterman, Gerda H
; APPLICANT: Jakob, Peter
; APPLICANT: Stuber, Dietrich
; TITLE OF INVENTION: Process for Producing Hydrophobic
; TITLE OF INVENTION: Polypeptides and Proteins, and Fusion Proteins for Use in
; TITLE OF INVENTION: Producing Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,348A
; FILING DATE: 29-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93110755.1
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parise, John P.
; REGISTRATION NUMBER: 34,403
; REFERENCE/DOCKET NUMBER: 4105/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6326
; TELEFAX: (201) 235-3500
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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 520 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 115..516
;     OTHER INFORMATION: /product= "Amyloid Protein AA"
US-08-268-348A-9

alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-268-348A-9  ..
Align seg 1/1 to: US-08-268-348A-9 from: 1 to: 520

1 AspalagluPheArghHisAspSerGlyTyrGluValHisGlnLys 16
|||||
388 GATCGGAGTTCGTCATGATTCAGGCTATGAAGTCCACCATCAAAAA 435

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-480-498-3

seq_documentation_block:
; Sequence 3, Application US/08480498
; Patent No. 5744346
; GENERAL INFORMATION:
;   APPLICANT: Chrysler, Susanna M.S.
;   APPLICANT: Sinha, Sukanto
;   APPLICANT: Keim, Pamela S.
;   APPLICANT: Anderson, John P.
;   TITLE OF INVENTION: Beta-Secretase
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Townsend and Townsend Kourie and Crew
;   STREET: One Market Plaza, Steuart Tower, Suite 2000
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94105
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/480,498
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Heslin, James M.
;   REGISTRATION NUMBER: 29,541
;   REFERENCE/DOCKET NUMBER: 015270-002200
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-326-2400
;   TELEFAX: 415-326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1521 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
US-08-480-498-3
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alignment_scores:
  Quality: 92.00      Length: 16
  Ratio: 5.750       Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x US-08-480-498-3  ..
Align seg 1/1 to: US-08-480-498-3 from: 1 to: 1521

1 AspalagluPheArghHisAspSerGlyTyrGluValHisGlnLys 16
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1222 GATGCAGAAATCCGACATGACTCAGGATATGAAGTTCATCAAAAA 1269
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us-09-155-076-2_1.rni

Wed Sep 13 08:11:41 2000

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:22:33 ; Search time 18.63 Seconds
(without alignments)
53.148 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92

Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_64.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	42	2 PNO512	beta-amyloid prote
2	92	100.0	57	2 E60045	Alzheimer's diseas
3	92	100.0	57	2 F60045	Alzheimer's diseas
4	92	100.0	57	2 G60045	Alzheimer's diseas
5	92	100.0	57	2 D60045	Alzheimer's diseas
6	92	100.0	57	2 A60045	Alzheimer's diseas
7	92	100.0	57	2 B60045	Alzheimer's diseas
8	92	100.0	82	2 P00438	Alzheimer's diseas
9	92	100.0	695	1 A49795	Alzheimer's diseas
10	92	100.0	770	1 QRH044	Alzheimer's diseas
11	77	93.7	747	2 JH0773	Alzheimer's diseas
12	73	79.3	33	2 S23094	Alzheimer's diseas
13	73	79.3	695	2 A27485	Alzheimer's diseas
14	73	79.3	695	2 S00550	Alzheimer's diseas
15	50.5	54.9	284	2 S04723	Alzheimer's diseas
16	50.5	54.9	327	2 S11435	genome polyprotein
17	50.5	54.9	519	2 FC1072	genome polyprotein
18	50.5	54.9	1555	2 JH0959	nuclear inclusion
19	49.5	53.8	971	2 D70128	polyprotein - pota
20	48.5	52.7	330	2 A26205	conserved hypothet
21	48.5	52.7	3063	2 JS0166	coat protein precu
22	45.5	49.5	313	2 JH0960	genome polyprotein
23	45.5	49.5	427	2 JA0073	polyprotein - pota
24	44	47.8	274	2 A64978	genome polyprotein
25	43	46.7	629	2 S60385	hypothetical prote
26	42.5	46.2	539	2 T39150	probable membrane
27	42	45.7	113	2 A64064	probable heat choc
28	42	45.7	373	2 D64971	ferredoxin [2Fe-2S
29	42	45.7	373	2 S28470	GDP-d-mannose dehy
					ribD protein - Vib

30 42 45.7 392 2 T19869 hypothetical prote
31 42 45.7 667 2 S64915 EMP70 protein prec
32 42 45.7 1240 2 S21086 anion exchange pro
33 41 44.6 182 2 S33992 finger protein ZNF
34 41 44.6 213 2 S43723 lactase (EC 3.2.1.
35 41 44.6 213 2 S43721 lactase (EC 3.2.1.
36 41 44.6 213 2 S43722 lactase (EC 3.2.1.
37 41 44.6 367 2 T39353 lactase (EC 3.2.1.
38 41 44.6 494 2 C70940 probable splicing
39 41 44.6 527 2 A43938 probable cobq prot
40 41 44.6 672 2 S52673 Pseudomonas cytoch
41 41 44.6 1918 2 S43719 probable membrane
42 41 44.6 1920 2 S43720 lactase (EC 3.2.1.
43 41 44.6 1926 2 S01169 lactase (EC 3.2.1.
44 40.5 44.0 559 2 F71420 beta-glycosidase c
45 40 43.5 155 2 T20945 hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

PNO512

beta-amyloid protein - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PNO512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A:Reference number: PNO512; MUID:93290653

A:Accession: PNO512

A:Molecule type: protein

A:Residues: 1-42 <SHI>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 92; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 1.5e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 92; DB 2; Length 57;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 6 DAEFRHDSGYEVHHQK 21

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Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
    |||||
DB 6 DAEFRHDSGYEVHHQK 21

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
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DB 6 DAEFRHDSGYEVHHQK 21

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match      100.0%; Score 92; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
    |||||
DB 6 DAEFRHDSGYEVHHQK 21

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180

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A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 92; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. NO. 3.2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16
 |||||
 Db 17 DAEFRHDSGYEVHOK 32

RESULT 9
 A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M56727; NID:g342062; PIDN:AAA36829.1; PID:g342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 100.0%; Score 92; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. NO. 3.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOK 16
 |||||
 Db 597 DAEFRHDSGYEVHOK 612

RESULT 10
 QRH04
 Alzheimer's disease amyloid beta protein precursor - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 24-Nov-1999
 C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
 4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
 A:Note: alternative splice form APP(695)
 R:La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LA>
 A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAAC13654.1; PID:g516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshihaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-770 <VOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <VOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
 R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-299, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Du
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemo
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzhe
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukula, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for t

A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S43135; NID:g257378; PIDN:AB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIRP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family IIT
A:Note: sequence extracted from NCBI backbone (NCBIRP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>

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A;Residues: 1-284 <BRA>
A;Cross-references: EMBL:XL14136; NID:g61445; PIDN:CAA32356.1; PID:g61446
C;Superfamily: tobacco etch virus genome polyprotein; DEAD/H box helicase homology
C;Keywords: polyprotein

Query Match 54.9%; Score 50.5; DB 2; Length 284;
Best Local Similarity 73.3%; Pred. No. 0.68;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
| | | | |
Db 4 DDEFEDS-YEVHHQ 17

Search completed: September 13, 2000, 02:22:34
Job time: 132 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:31 ; Search time 10.66 Seconds
(without alignments)
46.513 Million cell updates/sec

Title: US-09-155-076-2

Perfect score: 92

Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	92	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	92	100.0	57	1 A4_URUMA	Q29149 ursus marit
3	92	100.0	58	1 A4_CANFA	Q28280 canis famil
4	92	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	92	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	92	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	92	100.0	751	1 A4_SALSC	Q285241 saimiri sci
8	92	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	73	79.3	770	1 A4_MOUSE	P12023 mus musculu
10	73	79.3	770	1 A4_RAT	P11897 rattus norv
11	50.5	54.9	284	1 POLG_PVYVO	P08592 potatato viru
12	50.5	54.9	327	1 POLG_PVYCH	P21294 potatato viru
13	49.5	53.8	971	1 Y228_BORBU	O51246 borrelia bu
14	48.5	52.7	330	1 COAT_PENV	P07993 pepper mott
15	48.5	52.7	3063	1 POLG_PVYN	P18247 p genome po
16	44	47.8	274	1 YOHM_ECOLI	P76425 escherichia
17	43	46.7	629	1 FER7_YEAST	Q12333 saccharomyc
18	42	45.7	112	1 FER7_HAETN	P44428 haemophilus
19	42	45.7	315	1 HXB1_CYPCA	Q30346 cyprinus ca
20	42	45.7	373	1 GM4D_ECOLI	P32054 escherichia
21	42	45.7	667	1 EM70_YEAST	P32802 saccharomyc
22	42	45.7	1240	1 B3A2_HUMAN	P04920 homo sapien
23	41	44.6	494	1 COBQ_MYCTU	O53677 mycobacteri
24	41	44.6	848	1 Y233A_HUMAN	Q06730 homo sapien
25	41	44.6	1926	1 LPH_RABIT	P09849 oryctolagus
26	40	43.5	403	1 NOF2_DROME	P15297 drosophila
27	40	43.5	418	1 MTM1_MORSP	P11408 moraxella s
28	40	43.5	730	1 CATR_ASPNG	P35303 aspergillus
29	40	43.5	984	1 NOF_DROME	P16320 drosophila
30	39.5	42.9	3061	1 POLG_PVYHU	Q02963 p genome po
31	39	42.4	182	1 Y4YS_RHISN	P55727 rhizobium s
32	39	42.4	372	1 GM4D_YEREN	Q56872 yersinia en
33	38	41.3	260	1 RS4_YEAST	P05753 saccharomyc

34	38	41.3	372	1	GM4D_VIBCH	Q56598 vibrio chol
35	38	41.3	492	1	CAT1_TOBAC	P49319 nicotiana t
36	38	41.3	630	1	HCYA_EURCA	P14750 eurypelma c
37	38	41.3	955	1	VP2_BT17	P05309 bluetongue
38	38	41.3	1398	1	M3P1_YEAST	P43638 saccharomyc
39	37.5	40.8	506	1	2157_HUMAN	P51786 homo sapien
40	37.5	40.8	653	1	YDCP_ECOLI	P76104 escherichia
41	37	40.2	131	1	DLX4_ELECQ	P87394 eleutheroda
42	37	40.2	208	1	YIMA_STRCO	Q04296 streptomyce
43	37	40.2	351	1	NIFV_FRAAL	Q47884 frankia aln
44	37	40.2	401	1	NIFV_FRAAP	P54610 frankia sp.
45	37	40.2	489	1	YEN5_YEAST	P39970 saccharomyc

ALIGNMENTS

RESULT 1
A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
SEQUENCE FROM N.A.
RP TISSUE-BRAIN.
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:399-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56127; CAA39592.1; -.
CC HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;
DR EMBL; X56127; CAA39592.1; -.
DR HSSP; P05067; IAML.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33
FT TRANSMEM 34 57
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D98EBA82DFA CRC64;

Query Match 100.0%; Score 92; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

|||||

Db 6 DAEFRHDSGYEVHHQK 21

Wed Sep 13 08:11:42 2000

us-09-155-076-2_1.rsp

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RESULT 2
A4_URMSA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Thalarchos.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CRA39593.1; -.
CC HSP; P05067; IAML.
CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57
CC NON_TER 57
CC SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
CC
CC Query Match 100.0%; Score 92; DB 1; Length 57;
CC Best Local Similarity 100.0%; Pred. No. 1.8e-08;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC DB 6 DAEFRHDSGYEVHHQK 21
CC
CC RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

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[1]
RN SEQUENCE FROM N.A.
RP TISSUE-KIDNEY;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC -----
CC EMBL; X56125; CRA39590.1; -.
CC HSP; P05067; IAML.
CC PROSITE; PS00319; A4 EXTRA; PARTIAL.
CC PROSITE; PS00320; A4 INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1
CC CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 35 58
CC NON_TER 58
CC SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
CC
CC Query Match 100.0%; Score 92; DB 1; Length 58;
CC Best Local Similarity 100.0%; Pred. No. 1.8e-08;
CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 DAEFRHDSGYEVHHQK 16
CC DB 7 DAEFRHDSGYEVHHQK 22
CC
CC RESULT 4
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
DE PROTEIN (BETA-APP)] (FRAGMENT).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE; 92017079.
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
RT peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis";
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC

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 CC -----

DR EMBL; X56129; CAA39594.1; -
 DR HSP; P05067; IAML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 34 57
 FT DOMAIN 58 >58
 FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 5

A4_SHEEP
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
 DE PROTEIN (BETA-APP)] (FRAGMENT).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE; 92017079.

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC -----

DR EMBL; X56130; CAA39595.1; -
 DR HSP; P05067; IAML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 34 57
 FT DOMAIN 58 >58
 FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 Db 6 DAEFRHDSGYEVHHQK 21

RESULT 6

A4_BOVIN
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG [CONTAINS: BETA-AMYLOID
 DE PROTEIN (BETA-APP)] (FRAGMENT).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 92017079.

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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 CC -----

DR EMBL; X56124; CAA39589.1; -
 DR EMBL; X56126; CAA39591.1; -
 DR HSP; P05067; IAML.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 35 58
 FT DOMAIN 59 >59
 FT NON_TER 59 59 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 100.0%; Score 92; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Wed Sep 13 08:11:42 2000

us-09-155-076-2_1.rsp

OY 1 DAEFRHDSGYEVHOK 16
 DB 7 DAEFRHDSGYEVHOK 22

RESULT 7
 A4_SAISC STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR [CONTAINS: BETA-AMYLLOID PROTEIN (BETA-APP)].
 GN APP.
 OS Saimiri sclerous (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER, AND KIDNEY;
 RX MEDLINE; 96108492.
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC EMBL; S81024; AAD14347.1;
 DR FRAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PRINTS; PR00759; BASICPTASE.
 DR PROSITE; PS00280; BPTI_KUNITZ; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL);
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT CARBOHYD 523 523 PROBABLE.
 FT CARBOHYD 552 552 PROBABLE.
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 302 BY SIMILARITY.
 FT DISULFID 300 321 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 100.0%; Score 92; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 2,7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHOK 16

DB 653 DAEFRHDSGYEVHOK 668
 RESULT 8
 A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APPI) [CONTAINS: BETA-AMYLLOID PROTEIN (BETA-APP)].
 GN APP OR A4 OR CVAP OR ADL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE; 87144572.
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.";
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88122639.
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.";
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89128427.
 RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.";
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97263807.
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE; 88122640.
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L., Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE; 88122641.
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE; 87231971.
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).

RN [8] SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE: 88124954.
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE: 88035004.
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE: 90236318.
 RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furiya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE: 89016647.
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE: 87250462.
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE: 89384866.
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE: 90211252.
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE: 93188965.
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE: 99215582.
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN [17]

RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE: 91104913.
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE: 92031488.
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE: 94281210.
 RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE: 97128622.
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE: 98359783.
 RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN [22]
 RP STRUCTURE BY NMR OF 672-699.
 RA Poulsen S.A., Watson A.A., Craik D.J.;
 RT Submitted (JUN-1998) to the PDB data bank.
 RN [23]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE: 88296437.
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RL EMBO J. 7:949-957(1988).
 RN [24]
 RP REVIEW.
 RX MEDLINE: 92271194.
 RA Kosik K.S.;
 RT "Alzheimer's disease: a cell biological perspective.";
 RL Science 256:780-783(1992).
 RN [25]
 RP REVIEW ON VARIANTS.
 RX MEDLINE: 93250996.
 RA Hardy J.;
 RT "Framing beta-amyloid.";
 RL Nat. Genet. 1:233-234(1992).
 RN [26]
 RP Query Match 100.0% Score 92; DB 1; Length 770;
 Best Local Similarity 100.0% Pred. No. 2.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHOK 16
 Db 672 DAEFRHDSGYEVHOK 687
 |||||
 RESULT 9
 A4_MOUSE
 ID A4_MOUSE STANDARD; PRT; 770 AA.

AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE; 92096458.
 RA "The amyloid beta protein precursor or protease nexin II from mouse
 RT is closer related to its human homolog than previously reported."
 RL Biochem. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 88106489.
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RL protein precursor.";
 RN Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-PLACENTA;
 RX MEDLINE; 89345111.
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RL precursor of Mus domesticus.";
 RN Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE; 92209998.
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RN Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-BRAIN, AND KIDNEY;
 RX MEDLINE; 89149813.
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RL for the mouse homolog of Alzheimer's disease amyloid beta protein
 RC precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SURCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: SIX FORMS OF APP ARE FOUND; APP(395),
 CC APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); WHICH ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: APP(751) AND APP(770) CONTAIN A PROTEASE INHIBITOR
 CC DOMAIN BELONGING TO THE BPTI/KUNITZ FAMILY OF INHIBITORS.
 CC -----
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CC EMBL; X59379; -- NOT_ANNOTATED_CDS.
 DR EMBL; M18373; AAA37139.1; --
 DR EMBL; X15210; CAA3280.1; --
 DR EMBL; D10603; BAA01456.1; --
 DR EMBL; M24397; AAA39929.1; --
 DR PIR; A27485; A27485.
 DR PIR; S04855; S04855.
 DR PIR; S19727; S19727.
 DR MGD; MGI:88059; APP.
 DR PFAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PRINTS; PRO0204; BETAAMYLOID.
 DR PRINTS; PRO0759; BASICPTASE.
 DR PROSITE; PS00280; BPTI_KUNITZ; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT DOMAIN 18 599
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPLIC 289 289
 FT VARSPLIC 290 364
 FT VARSPLIC 346 380
 FT VARSPLIC 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;
 QY 1 DAEFRHDSGVEVHHOK 16
 DB 672 DAEFGHDSGFEVHHOK 687
 Query Match 79.3%; Score 73; DB 1; Length 770;
 Best Local Similarity 81.2%; Pred. No. 0.0003;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 RESULT 10
 ID A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR
 DE (AMYLOIDOGENIC GLYCOPROTEIN) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 88312583.
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RL in rat brain suggests a role in cell contact.";
 RN EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=LIVER;

Wed Sep 13 08:11:42 2000

us-09-155-076-2_1.rsp

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CC EMBL; X54058; CAA37993.1; -.
DR PIR; S11549; S11549.
DR HSP; P05067; IAMB.
DR PFAM; PF00767; Poty_coat; 1.
KW Transferase; RNA-directed RNA polymerase; Coat protein; Polyprotein.
FT NON_TER 1
FT CHAIN <1 60 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 61 327 COAT PROTEIN.
SQ SEQUENCE 327 AA; 36868 MW; 8f8355E2DE6F2F18 CRC64;

Query Match 54.9%; Score 50.5; DB 1; Length 327;
Best Local Similarity 73.3%; Pred. No. 0.47;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
DB 47 DDEFEFDS-YEVHHQ 60

RESULT 13
V228_BORBU STANDARD; PRT; 971 AA.
ID Y228_BORBU
AC OS1246;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL PROTEIN BB0228.
GN BB0228
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE; 98065943.
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RA "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).

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CC EMBL; AE001133; AAC66621.1; -.
DR TIGR; BB0228; -.
KW Hypothetical protein.
SQ SEQUENCE 971 AA; 112959 MW; 088A688D7B8C591A CRC64;

Query Match 53.8%; Score 49.5; DB 1; Length 971;
Best Local Similarity 57.9%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 DAE---FRHDSGYEVHHQ 16
DB 19 DAEGYFKHESGIEVFLK 37

RESULT 14
COAT_PEMV

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ID COAT_PEMV STANDARD; PRT; 330 AA.
AC P07993;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE COAT PROTEIN.
OS Pepper mottle virus (PeMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RA Dougherty W.G., Allison R.F., Parks T.D., Johnston R.E., Feild M.J.,
RA Armstrong F.B.;
RT "Nucleotide sequence at the 3' terminus of pepper mottle virus
RT genomic RNA: evidence for an alternative mode of potyvirus capsid
RT protein gene organization.";
RL Virology 146:282-291(1985).

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CC EMBL; M11598; AAA46902.1; -.
DR PIR; A26205; A26205.
DR PFAM; PF00767; Poty_coat; 1.
KW Coat protein.
SQ SEQUENCE 330 AA; 37028 MW; C63A2F810D95820E CRC64;

Query Match 52.7%; Score 48.5; DB 1; Length 330;
Best Local Similarity 73.3%; Pred. No. 0.99;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
DB 50 DDEFEFDS-YEVHHQ 63

RESULT 15
POLG_PVYN STANDARD; PRT; 3063 AA.
ID POLG_PVYN
AC P18247; Q85266; Q85267; Q85268; Q85269; Q85270; Q85271; Q85272;
AC Q85273;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 6 KDA PROTEIN 2 (6K2);
DE 1 (SK1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89279275.
RA Robaglia C., Durand-Tardif M., Tronchet M., Boudasin G.,
RA Astier-Manificier S., Casse-Delbart F.;
RT "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";
RL J. Gen. Virol. 70:935-947(1989).
RN [2]
RP REVISIONS.
RA Durand-Tardif M.;
RA Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.

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CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- FPM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- FPM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
CC -----
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CC -----
CC EMBL: X12456; CAA30988.1; -;
CC EMBL: D00441; BAA0342.1; -;
CC PIR: JS0166; JS0166.
CC PFAM: PF00270; DEAD; 1.
CC PFAM: PF00863; Peptidase_C4; 1.
CC PFAM: PF00851; Peptidase_C6; 1.
CC PFAM: PF01577; Poty_P1; 1.
CC PFAM: PF00767; Poty_coat; 1.
CC PFAM: PF00680; RNA_dep_RNA_pol; 1.
CC PFAM: PF00271; helicase_C; 1.
CC PRINTS: PR00966; NIAPOTYPTASE.
CC Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
CC ATP-binding.
CC CHAIN 1 275 N-TERMINAL PROTEIN.
CC CHAIN 276 824 HELPER COMPONENT PROTEINASE.
CC CHAIN 825 ? PROTEIN P3.
CC CHAIN ? 1157 6 kDa PROTEIN 1.
CC CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
CC CHAIN 1792 1843 6 kDa PROTEIN 2.
CC CHAIN 1844 ? GENOME-LINKED PROTEIN.
CC CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
CC CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.
CC CHAIN 2797 3063 COAT PROTEIN.
CC BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
CC SIMILARITY).
CC FT NP_BIND 1242 1249 ATP (POTENTIAL).
CC SEQUENCE 3063 AA; 347535 MW; 3EC79125DE33F1BB CRC64;

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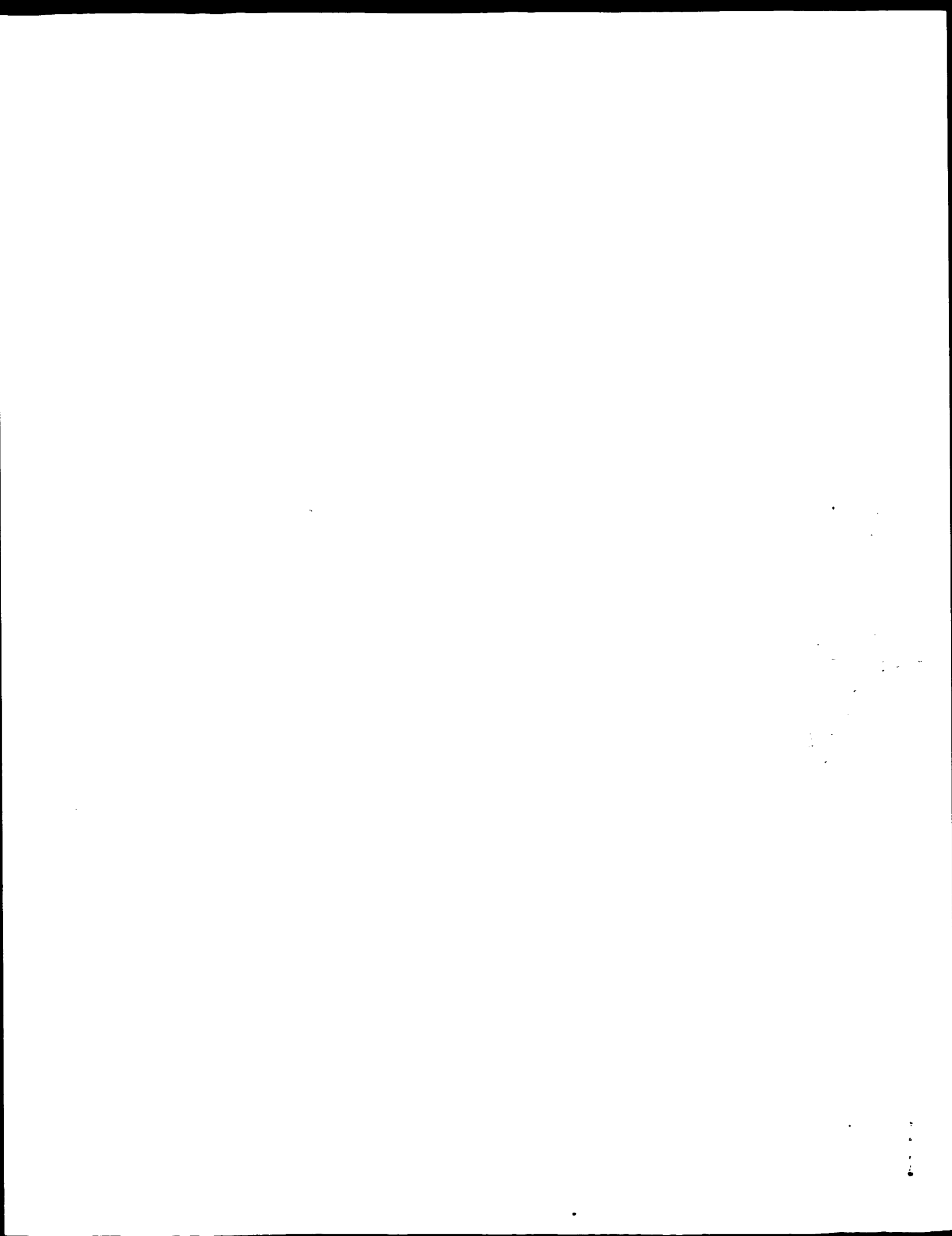
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Query Match 52.7%; Score 48.5; DB 1; Length 3063;
Best Local Similarity 73.3%; Pred. No. 10;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
   ||| |||||
Db 2783 DDEEELDS-YEVHHQ 2796

```

Search completed: September 13, 2000, 02:24:32
Job time: 170 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 13, 2000, 02:24:09 ; Search time 22.49 seconds
(without alignments)
49.326 Million cell updates/sec

Title: US-09-155-076-2
Perfect score: 92
Sequence: 1 DAEFRHDSGYEVHHQK 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_12:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	100.0	82	4 Q16020	Q16020 homo sapien
2	92	100.0	82	4 Q16019	Q16019 homo sapien
3	92	100.0	82	4 Q16014	Q16014 homo sapien
4	92	100.0	82	4 P78438	P78438 homo sapien
5	92	100.0	534	13 Q93296	Q93296 gallus gall
6	92	100.0	695	11 Q60496	Q60496 cavia porce
7	82	89.1	97	4 Q13778	Q13778 homo sapien
8	77	83.7	747	13 Q91963	Q91963 xenopus lae
9	73	79.3	79	11 Q35463	Q35463 cricetus lae
10	73	79.3	695	11 P97487	P97487 mus musculu
11	72	78.3	699	13 Q57394	Q57394 narke japon
12	50.5	54.9	292	12 Q85276	Q85276 potato viru
13	50.5	54.9	365	12 Q9WG05	Q9WG05 potato viru
14	50.5	54.9	1555	12 Q85274	Q85274 potato viru
15	50	54.3	780	13 Q73683	Q73683 tetraodon f
16	49	53.3	737	13 Q93279	Q93279 fugu rubrip
17	47	51.1	205	2 Q44945	Q44945 borrelia bu
18	46	50.0	372	2 Q85339	Q85339 escherichia
19	45.5	49.5	313	12 Q85259	Q85259 potato viru

20	45.5	49.5	976	12	Q85104	Q85104 potato viru
21	45.5	49.5	3061	12	Q85265	Q85265 potato viru
22	44.5	48.4	519	12	Q72606	Q72606 potato viru
23	44.5	48.4	3081	12	Q85105	Q85105 potato viru
24	44	47.8	297	2	Q92NCL	Q92NCL nitrosomona
25	42.5	46.2	539	3	Q14283	Q14283 schizosacch
26	42	45.7	339	4	Q75357	Q75357 homo sapien
27	42	45.7	372	4	Q60547	Q60547 homo sapien
28	42	45.7	373	2	Q06952	Q06952 vibrio chol
29	42	45.7	667	3	Q12101	Q12101 saccharomyc
30	41	44.6	213	6	Q29520	Q29520 oryctolagus
31	41	44.6	213	6	Q29522	Q29522 oryctolagus
32	41	44.6	213	6	Q29521	Q29521 oryctolagus
33	41	44.6	356	10	Q22331	Q22331 hevea brasl
34	41	44.6	367	3	Q43120	Q43120 schizosacch
35	41	44.6	494	2	Q53677	Q53677 mycobacteri
36	41	44.6	551	2	Q52519	Q52519 pseudomonas
37	41	44.6	672	3	Q04562	Q04562 saccharomyc
38	41	44.6	944	4	Q14697	Q14697 homo sapien
39	41	44.6	966	11	Q08794	Q08794 mus musculu
40	41	44.6	1919	6	Q29518	Q29518 oryctolagus
41	41	44.6	1920	6	Q29519	Q29519 oryctolagus
42	40.5	44.0	559	10	Q23409	Q23409 arabidopsis
43	40	43.5	104	2	Q925P5	Q925P5 enterococcu
44	40	43.5	155	5	Q19475	Q19475 caenorhabdi
45	40	43.5	311	10	Q39500	Q39500 cylindroche

ALIGNMENTS

RESULT 1
Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
RT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93236601.
RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; CAB32008.1; -
DR HSSP: P05067; IAML.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8882 MW; 55734509 CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||
Db 18 DAEFRHDSGYEVHHQK 33

RESULT 2
Q16019 PRELIMINARY; PRT; 82 AA.
ID Q16019
AC Q16019;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
RT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236601.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

mutations on the processing of the beta-amyloid peptide precursor."

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S61380; CAB32007.1; -.

DR HSSP; P05067; IAML.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8938 MW; 4C8B0E6E CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 18 DAEFRHDSGYEVHHQK 33

RESULT 3

Q16014

TID Q16014 PRELIMINARY; PRT; 82 AA.

AC Q16014;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE BETA-AMYLLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93236601.

RA DENMAN R.B., ROSENZWAIG R., MILLER D.L.;

RT "A system for studying the effect(s) of familial Alzheimer disease

mutations on the processing of the beta-amyloid peptide precursor."

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).

DR EMBL; S60721; CAB31888.1; -.

DR HSSP; P05067; IAML.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 8972 MW; 30147E4F CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 18 DAEFRHDSGYEVHHQK 33

RESULT 4

P78438

ID P78438 PRELIMINARY; PRT; 82 AA.

AC P78438;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE AMYLLOID PROTEIN (BETA-AMYLLOID PROTEIN) (FRAGMENT).

GN APP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 8932030.
 RA JOHNSTONE E.M., CHANEY M.O., MOORE R.E., WARD K.E., NORRIS F.H.,
 RA LITTLE S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [2]
 RP SEQUENCE OF 19-48 FROM N.A.
 RX MEDLINE; 87120329.
 RA TANZI R.E., GUSELLA J.F., WATKINS P.C., BRUNS G.A., GEORGE-HYSLOP P.,
 RA VAN KEUREN M.L., PATTERSON D., PAGAN S., KURNIT D.M., NEVE R.L.;
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
 RT linkage near the Alzheimer locus."
 RL Science 235:880-884(1987).
 RN [3]
 RP SEQUENCE OF 32-63 FROM N.A.
 RX MEDLINE; 93035397.
 RA KAMINO K., ORR H.T., PAYAMI H., WIJSMAN E.M., ALONSO M.E., PULST S.M.,
 RA ANDERSON L., O'DAHL S., NEMENS E., WHITE J.A.;
 RT "Linkage and mutational analysis of familial Alzheimer disease
 RT kindreds for the APP gene region."
 RL Am. J. Hum. Genet. 51:998-1014(1992).
 DR EMBL; M29270; AAA51768.1; -.
 DR EMBL; M29269; AAA51768.1; JOINED.
 DR EMBL; M15532; AAA51564.1; -.
 DR EMBL; S45136; AAB23646.1; -.
 DR HSSP; P05067; IAML.
 FT NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8994 MW; 5399FFA4 CRC32;

Query Match 100.0%; Score 92; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 17 DAEFRHDSGYEVHHQK 32

RESULT 5

O93296

ID O93296 PRELIMINARY; PRT; 534 AA.

AC O93296;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE AMYLLOID PRECURSOR PROTEIN (FRAGMENT).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;

OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RA BARNES N.Y., LING L., YOSHIKAWA K., SCHWARTZ L.M., OPPENHEIM R.W.,

RA MILLIGAN C.E.;

RT "Increased production of amyloid precursor protein provides a

substrate for Caspase 3 in dying motoneurons."

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF042098; AAC25052.1; -.

DR HSSP; P05067; IAML.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1

SQ SEQUENCE 534 AA; 60597 MW; 6F117D2F CRC32;

Query Match 100.0%; Score 92; DB 13; Length 534;

Best Local Similarity 100.0%; Pred. No. 3.5e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

Db 17 DAEFRHDSGYEVHHQK 32

Db 436 DAEFRHDSGYEVHHQK 451

RESULT 6

Q60496 PRELIMINARY; PRT; 695 AA.

AC Q60496;

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)

DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RA BECK M., MUELLER D., BIGL V.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -!- SIMILARITY: TO OTHER SPECIES APP ANALOGUES.

DR EMBL; X97631; CAA66230.1; -.

DR HSSP; P05067; 1AML.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00204; BETAMAMYL0ID.

DR PRINTS; PR00204; BETAMAMYL0ID.

SQ SEQUENCE 695 AA; 78701 MW; CE050651 CRC32;

Query Match 100.0%; Score 92; DB 11; Length 695;

Best Local Similarity 100.0%; Pred. No. 4.6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 597 DAEFRHDSGYEVHHQK 612

RESULT 7

Q13778 PRELIMINARY; PRT; 97 AA.

AC Q13778;

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)

DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE; 87120328.

RA GOLDGABER D., LERMAN M.I., MCBRIDE O.W., SAFFIOTTI U., GAJDUSEK D.C.;

RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.";

RL Science 235:877-880(1987).

DR EMBL; M15533; AAA35540.1; -.

DR HSSP; P05067; 1AML.

FT NON_TER 1

SQ SEQUENCE 97 AA; 10884 MW; C4D32AA2 CRC32;

Query Match 89.1%; Score 82; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 2.4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHHQK 16

DB 1 EFRHDSGYEVHHQK 14

RESULT 8

Q91963 PRELIMINARY; PRT; 747 AA.

AC Q91963;

DT 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)

DE APP747.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;

OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;

OC Xenopus.

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE; 93129227.

RA OKADO H., OKAMOTO H.;

RT "A Xenopus homologue of the human beta-amyloid precursor protein: RT developmental regulation of its gene expression.";

RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).

DR EMBL; S52417; AAB24853.1; -.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PFAM; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00204; BETAMAMYL0ID.

DR PRINTS; PR00759; BASICPTASE.

KW Serine protease inhibitor.

SQ SEQUENCE 747 AA; 84892 MW; A7580143 CRC32;

Query Match 83.7%; Score 77; DB 13; Length 747;

Best Local Similarity 75.0%; Pred. No. 0.00013;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 649 DSEYRHDATAYEVHHQK 664

RESULT 9

O35463 PRELIMINARY; PRT; 79 AA.

AC O35463;

DT 01-JAN-1998 (TREMELrel. 05, Created)

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)

DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)

DE ALZHEIMER'S AMYLOID BETA PROTEIN PRECURSOR (FRAGMENT).

GN BETA APP.

OS Cricetulus griseus (Chinese hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae; Cricetulus.

RN [1]

RP SEQUENCE FROM N.A.

RA SAMBAMURTI K., PINNIX I., GANDHI S.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF030413; AAB86608.1; -.

DR HSSP; P05067; 1QCM.

FT NON_TER 1

FT NON_TER 79

SQ SEQUENCE 79 AA; 8538 MW; EB3BB61F CRC32;

Query Match 79.3%; Score 73; DB 11; Length 79;

Best Local Similarity 81.2%; Pred. No. 5.5e-05;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16

DB 21 DAEFGHDSGFEVHHQK 36

RESULT 10

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P97487
ID P97487 PRELIMINARY; PRT; 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAMP8; TISSUE-HIPPOCAMPUS;
RA FLOOD J.F., KUMAR V.B., SASSER T., WORD I., MORLEY J.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN-129SV;
RA WRAGG M.A., BUSFIELD F., DUFF K., KORENBLAT K., CAPECCHI M.,
RA LORING J.F., GOATE A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84012; AAB41502.1; -
DR EMBL; U83624; AAB40919.1; -
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PRINTS; PRO0203; AMYLOIDM4.
DR PRINTS; PRO0204; BETAAMYLOID.
SQ SEQUENCE 695 AA; 78414 MW; B709D560 CRC32;

Query Match 79.3%; Score 73; DB 11; Length 695;
Best Local Similarity 81.2%; Pred. No. 0.00054;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQ 16
| | | | | | | | | | | | | | | | | |
DB 597 DAEFGHDSGFVHHQ 612

RESULT 11
Q57394 PRELIMINARY; PRT; 699 AA.
AC Q57394;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE EL AMYLOID PRECURSOR PROTEIN 699.
GN EL APP699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Rajiformes; Narke.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ELECTRIC LOBE;
RA IJIMA K., LEE D., OKUTSU J., TOMITA S., HIRASHIMA N., KIRINO Y.,
RA SUZUKI T.;
RL Biochem. J. 0:0-0(1998).
DR EMBL; AB005544; BAA24230.1; -
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PRINTS; PRO0203; AMYLOIDM4.
DR PRINTS; PRO0204; BETAAMYLOID.
SQ SEQUENCE 699 AA; 78879 MW; 11604C05 CRC32;

Query Match 78.3%; Score 72; DB 13; Length 699;
Best Local Similarity 75.0%; Pred. No. 0.00079;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQ 16
: | | | | | | | | | | | | | | | |
DB 601 ETEFGHDSGFVHHQ 616

P97487
ID P97487 PRELIMINARY; PRT; 292 AA.
AC Q85276;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RA GRIFFIN J.D., SHIEL P.S., BERGER P.H., THORNBURY D.W.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; M81435; AAA47185.1; -
DR PFAM; PF00767; Poty_coat; 1.
KW Polyprotein.
FT NON_TER 1 1 NIB.
FT CHAIN 26 292 COAT PROTEIN.
SQ SEQUENCE 292 AA; 32945 MW; 8CB34E72 CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 292;
Best Local Similarity 73.3%; Pred. No. 0.94;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
| | | | | | | | | | | | |
DB 12 DDEFEFDS-YEVHHQ 25

RESULT 13
Q9WG05 PRELIMINARY; PRT; 365 AA.
AC Q9WG05;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Potato virus Y.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORDINARY; O;
RA BHAT A.I., VARMA A., PAPPU H.R., RAJAMANNAR M., JAIN R.K., PRAVEEN S.;
RT "N-terminal serology and sequence relationships indicate that a
RT potyvirus from eggplant, Solanum melongena L., is a strain of potato
RT virus Y.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF118153; AAD24563.1; -
KW Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 365 AA; 41418 MW; F3CF9EBD CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 365;
Best Local Similarity 73.3%; Pred. No. 1.2;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
| | | | | | | | | | | | |
DB 85 DDEFEFDS-YEVHHQ 98

RESULT 14
Q85274 PRELIMINARY; PRT; 1555 AA.
ID Q85274
AC Q85274;

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DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE POLYPROTEIN (FRAGMENT).
 OS Potato virus Y.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O;
 RX MEDLINE; 92335011.
 RA HIDAKA M., YOSHIDA Y., MASAKI H., NAMBA S., YAMASHITA S.,
 RA TSUCHIZAKI T., UOZUMI T.;
 RT "Cloning and sequencing of the 3' half of a potato virus Y (O strain)
 RT genome encoding the 5k protein, protease, polymerase and coat
 RT protein.";
 RL Nucleic Acids Res. 20:3515-3515(1992).
 DR EMBL; D12539; BAA02107.1; .
 DR PFAM; PF00863; Peptidase_C4; 1.
 DR PFAM; PF00767; Poty_coat; 1.
 DR PFAM; PF00680; RNA_dep_RNA_pol; 1.
 KW Polyprotein; Coat protein; Protease.
 FT NON_TER 1
 FT CHAIN 1 285 CYTOPLASMIC INCLUSION BODY.
 FT CHAIN 286 337 5-KD PROTEIN.
 FT CHAIN 338 769 PROTEASE.
 FT CHAIN 770 1288 RNA POLYMERASE.
 FT CHAIN 1289 1555 COAT PROTEIN.
 SQ SEQUENCE 1555 AA; 176933 MW; 4403DDF0 CRC32;

Query Match 54.9%; Score 50.5; DB 12; Length 1555;
 Best Local Similarity 73.3%; Pred. No. 5.4;
 Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 DAEFRHDSGYEVHHQ 15
 DB 1275 DDEFEFDS-YEVHHQ 1288
 | | | | | | | | | |

RESULT 15
 073683
 ID 073683 PRELIMINARY; PRT; 780 AA.
 AC 073683;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE AMYLOID PRECURSOR PROTEIN.
 OS Tetraodon fluviatilis (Puffer fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98252138.
 RA VILLARD L., TASSONE F., CRNOGORAC-JURCEVIC T., CLANCY K., GARDINER K.;
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";
 RL Gene 210:17-24(1998).
 DR EMBL; AF018165; AAC41275.1; .
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PFAM; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PRINTS; PR00759; BASICPTASE.
 SQ SEQUENCE 780 AA; 88238 MW; 99DD89A8 CRC32;

Query Match 54.3%; Score 50; DB 13; Length 780;
 Best Local Similarity 56.2%; Pred. No. 3.2;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQ 16

Db 682 ETEDEQSTEEYEVHHQK 697
 : | | : | | | | |

Search completed: September 13, 2000, 02:24:10
 Job time: 178 sec

us-09-155-076-2_1.rspt

Wed Sep 13 08:11:43 2000

OM of: US-09-155-076-2 to: EST:* out_format : pfs

Date: Sep 13, 2000 2:42 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-C/CDN2_1/USPTO.spool/US09155076/runat_29082000_092504_15735/app_query.fasta_1.144
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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-DEEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
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Search information block:

Query: US-09-155-076-2

Query length: 16

Database: EST:*

Database sequences: 5247842

Database length: -2090053206

Search time (sec): 875.890000

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gb_est41:AA137593	-	92.00	280.72	8.3e-07	277
gb_est27:AA1909276	-	92.00	280.68	8.3e-07	278
gb_est5:AA303751	+	92.00	279.17	9.0e-07	297
gb_est47:FA06018	+	92.00	280.87	9.3e-07	305
gb_est44:AA580695	-	92.00	279.85	9.3e-07	306
gb_est26:AA1902528	-	92.00	279.05	1.0e-06	335
gb_est5:AA322074	+	92.00	278.98	1.0e-06	338
gb_est26:AA1902529	+	92.00	278.98	1.0e-06	338
gb_est5:AA304003	+	92.00	278.57	1.1e-06	334
gb_est52:TA99906	+	92.00	277.88	1.2e-06	333
gb_est51:RI19709	+	92.00	277.53	1.3e-06	339
gb_est2:AA134479	+	92.00	277.14	1.3e-06	417
gb_est16:AA1124771	+	92.00	276.26	1.5e-06	461
gb_est44:AA601576	+	92.00	276.11	1.5e-06	489
gb_est51:R25913	+	92.00	275.82	1.6e-06	485
gb_est3:AA218652	+	92.00	275.36	1.6e-06	511
gb_est44:AA602193	+	92.00	274.85	1.8e-06	542
gb_est45:AA6073480	+	92.00	273.87	2.0e-06	606
gb_est2:AA082598	+	92.00	273.80	2.0e-06	611
gb_est2:AA081869	+	92.00	273.66	2.1e-06	621
gb_est28:AA1980795	+	92.00	273.23	2.2e-06	652
gb_est41:AA362065	+	88.00	271.82	2.6e-06	284
gb_est44:AA361403	+	88.00	260.89	1.1e-05	647
gb_est44:AA607890	+	86.00	261.81	9.4e-06	286
gb_est44:AA608448	+	86.00	254.14	2.5e-05	688
gb_est5:AA299326	+	85.00	256.20	1.9e-05	381
gb_est41:AA364975	+	84.00	252.72	3.0e-05	398
gb_est28:AA046001	+	84.00	250.21	4.2e-05	530
gb_est1:AA029792	+	82.00	249.31	4.7e-05	289
gb_est1:AA034297	+	82.00	245.63	7.5e-05	440
gb_est44:AA608486	+	81.00	242.37	0.0001	639
gb_est44:AA577954	+	81.00	255.05	2.2e-05	105
gb_est54:W26339	-	76.00	222.66	0.0014	724
gb_est13:AA669182	+	73.00	222.96	0.0018	341
gb_est13:AA669182	+	73.00	220.93	0.0014	304
gb_est53:W13829	+	73.00	218.77	0.0023	389
gb_est2:AA074807	+	73.00	218.31	0.0025	410
gb_est13:AA914658	+	73.00	218.00	0.0026	425
gb_est24:AA171076	+	73.00	218.00	0.0026	425
gb_est7:AA462949	+	73.00	217.62	0.0027	444

gb_est15:AI045218 - 73.00 217.33 0.0028 459 ! AI045218 UI-R-Cl-ju-g-11-0-U
gb_est2:AA137593 + 73.00 217.16 0.0029 468 ! AA137593 mq28a02.r1 Barstead
gb_est41:AA321190 + 73.00 216.97 0.0029 478 ! AW321190 uc27a05.y1 NCI CGAP
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seq_documentation_block:

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DEFINITION EST99048 Thyroid Homo sapiens cDNA 5' end similar to amyloid, A4
beta subunit, mRNA sequence.
ACCESSION AA385402
VERSION AA385402.1 GI:2037720
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 246)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Buit,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 12140200

COMMENT

Other_ESTs: THC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse

Location/Qualifiers

1. .246

/organism="Homo sapiens"

/db_xref="ATCC (inhst):189572"

/db_xref="taxon:9606"

/clone_lib="Thyroid"

/dev_stage="adult"

/note="Organ: thyroid gland; Vector: pBluescript SK-;

Site:1: EcoRI; Site:2: XhoI"

BASE COUNT 70 a 48 c 68 g 58 t

ORIGIN

alignment_scores:

Quality: 92.00 Length: 16

Ratio: 5.750 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AA385402

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Align seg 1/1 to: AA385402 from: 1 to: 246

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
116 GATGAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 163

seq_name: gb_est41:AW379017

seq_documentation_block: 277 bp mRNA EST 04-FEB-2000
LOCUS AW379017
DEFINITION RC3-HT0230-241099-012-c12 HT0230 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379017
VERSION AW379017.1 GI:6883676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 277)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036339.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT0230-
241099-012-c12&t3=1999-10-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 277.
Location/Qualifiers
1..277
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0230"
/dev_stage="Adult"
/note="Organ: head/neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 70 a 79 c 51 g 77 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AW379017/rev ..
Align seg 1/1 to reverse of: AW379017 from: 1 to: 277

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
220 GATGAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 173

seq_name: gb_est27:AI909276

seq_documentation_block: 278 bp mRNA EST 30-MAR-2000
LOCUS AI909276
DEFINITION QV-BT202-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI909276
VERSION QV-BT202-070599-188 BT202 Homo sapiens cDNA, mRNA sequence.
KEYWORDS EST.
SOURCE human.

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```

ACCESSION AI909276
VERSION AI909276.1 GI:6499956
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 278)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-3496 (2000)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2284565.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seg/gethtml.pl?tl=QV&t2=QV-BT202-188.html
&t3=070599&t4=1)
Seq primer: puc 18 forward.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT202"
/sex="female"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 71 a 79 c 54 g 74 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-155-076-2 x AI909276/rev ..
Align seg 1/1 to reverse of: AI909276 from: 1 to: 278

1 AspaLaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
207 GATGAGAAATCCGACATGACTCAGGATATGAGTTCATCATCAAAA 160

seq_name: gb_est5:AA303751

seq_documentation_block: 297 bp mRNA EST 18-APR-1997
LOCUS AA303751
DEFINITION EST16434 Aorta endothelial cells, TNF alpha-treated Homo sapiens
CDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.
ACCESSION AA303751
VERSION AA303751.1 GI:1956103
KEYWORDS EST.
SOURCE human.

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
REFERENCE
ADAMS, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitchugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-P., Ferrite, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6347 Suppl), 3-174 (1995)
JOURNAL
MEDLINE
COMMENT
On Sep 29, 1997 this sequence version replaced gi:1520591.
Other ESTs: THCL72078
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@igr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source
1..297
/organism="Homo sapiens"
/db_xref="Arcc (inhost):115367"
/db_xref="taxon:9606"
/clone_lib="Aorta endothelial cells, TNF alpha-treated"
/cell_type="endothelial cell"
/dev_stage="adult"
/note="organ: aorta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT 79 a 71 c 79 g 67 t 1 others
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-2 x AA303751 ..
Align seg 1/1 to: AA303751 from: 1 to: 297

1 AspalagluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
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217 GATGAGATTCCGACATGACATGAGTATGAGTTCATCATCAAAA 264
seq_name: gb_est47:F06018

seq_documentation_block:
LOCUS F06018 305 bp mRNA EST 19-FEB-1995
DEFINITION HSC00A101 normalized infant brain cDNA Homo sapiens cDNA clone
c-Qual0, mRNA sequence.
ACCESSION F06018

VERSION F06018.1 GI:669834
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 305)
REFERENCE
AUFFRAY, C., Benar, G., Bois, F., Bouchier, C., da Silva, C.,
Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,
Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,
Sebastiani-Kabatchis, C. and Tessier, A.
IMAGE: molecular integration of the analysis of the human genome
and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
JOURNAL
MEDLINE
COMMENT
On May 20, 1999 this sequence version replaced gi:4878117.
Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
Email: genexpress@genethon.fr
Single read.
Genexpress.library.idt: C; Genexpress.sequence.idt: ylc-Qual0
Seq primer: (-21)M13 universal.

FEATURES
source
1..305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="c-Qual0"
/clone_lib="normalized infant brain cDNA"
/sex="Female"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site 1: HindIII;
Site 2: NotI; sex: Female; dev stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dt) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Souares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
BASE COUNT 88 a 65 c 80 g 71 t 1 others
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-155-076-2 x F06018 ..
Align seg 1/1 to: F06018 from: 1 to: 305

1 AspalagluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
3 GATGAGATTCCGACATGACATGAGTATGAGTTCATCATCAAAA 50
seq_name: gb_est44:AW580695

seq_documentation_block:
LOCUS AW580695 306 bp mRNA EST 16-MAR-2000
DEFINITION RC4-LT0011-100100-012-cl1 LT0011 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW580695
VERSION AW580695.1 GI:7255744
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Wed Sep 13 08:11:43 2000

REFERENCE 1 (bases 1 to 306)
 AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT On Jan 6, 2000 this sequence version replaced gi:5676947.

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4-LT0011-
 100100-012-cil&t3=2000-01-10&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 6
 High quality sequence stop: 306.

FEATURES
 source
 1..306
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="LT0011"
 /dev_stage="Adult"

/note="Organ: leiomyos; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 72 a 80 c 65 g 89 t
 ORIGIN

alignment_scores:
 Quality: 92.00 Length: 16
 Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-2 x AW580695/rev ..
 1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 188 GATGCAGAAATTCGACATGACTGAGTATGAGTTCATCATCAAAAA 141

Align seg 1/1 to reverse of: AW580695 from: 1 to: 306

seq_name: gb_est26:AI902528

seq_documentation_block:
 LOCUS AI902528 335 bp mRNA EST 30-MAR-2000
 DEFINITION QV-BT009-101198-075 BT009 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AI902528
 VERSION AI902528.1 GI:6492915
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 335)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zagó,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 TITLE
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

On May 18, 1998 this sequence version replaced gi:3138510.

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT009-075.html
 &t3=101198&t4=1)

Seq primer: puc 18 forward.

FEATURES
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 1..335
 Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BT009"

/sex="female"

/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

BASE COUNT 77 a 89 c 76 g 93 t
 ORIGIN

alignment_scores:
 Quality: 92.00 Length: 16
 Ratio: 5.750 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-155-076-2 x AI902528/rev ..

Align seg 1/1 to reverse of: AI902528 from: 1 to: 335

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
 312 GATGCAGAAATTCGACATGACTGAGTATGAGTTCATCATCAAAAA 265

seq_name: gb_est5:AA322074

seq_documentation_block:
 LOCUS AA322074 338 bp mRNA EST 19-APR-1997
 DEFINITION EST24653 Cerebellum II Homo sapiens cDNA 5' end similar to amyloid,
 A4 beta subunit, mRNA sequence.

ACCESSION AA322074

VERSION AA322074.1 GI:1974399

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 338)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gockayne,J.D.,
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
 Kelley,J.M., Kelley,J.C., Liu,J.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL
MEDLINE
COMMENT

Other_ESTs: THC172078

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse:

Location/Qualifiers

1. .338

/organism="Homo sapiens"

/db_xref="ATCC (inhost):122569"

/db_xref="taxon:9606"

/clone_lib="Cerebellum II"

/tissue_type="cerebellum"

/dev_stage="adult"

/note="Organ: brain; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI"

BASE COUNT 86 a 78 c 95 g 79 t

ORIGIN

alignment_scores:

Quality: 92.00

Ratio: 5.750

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 16

Gaps: 0

US-09-155-076-2 x AA322074 ..

Align seg 1/1 to: AA322074 from: 1 to: 338

1 AsplaglupeArGHisAspSerGlyTyrgluValHisHisGlnLys 16

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210 GATGAGAAATCCGACATGACTCAGGATGATGAGTTCATCATCAAAA 257

seq_name: gb_est26:AI902529

seq_documentation_block:

LOCUS AI902529 338 bp mRNA EST 30-MAR-2000

DEFINITION QV-BT009-101198-074 BT009 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI902529

VERSION AI902529.1 GI:6492916

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 338)

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

On Oct 30, 1998 this sequence version replaced gi:3814489.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

TITLE

JOURNAL

COMMENT

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT009-074.html>)

seq primer: puc 18 forward.

Location/Qualifiers

1. .338

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="BT009"

/sex="female"

/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 78 a 89 c 76 g 95 t

ORIGIN

alignment_scores:

Quality: 92.00

Ratio: 5.750

Percent Similarity: 100.000

Percent Identity: 100.000

Length: 16

Gaps: 0

US-09-155-076-2 x AI902529/rev ..

Align seg 1/1 to reverse of: AI902529 from: 1 to: 338

1 AsplaglupeArGHisAspSerGlyTyrgluValHisHisGlnLys 16

|||||

315 GATGAGAAATCCGACATGACTCAGGATGATGAGTTCATCATCAAAA 268

seq_name: gb_est5:AA304003

seq_documentation_block:

LOCUS AA304003 354 bp mRNA EST 18-APR-1997

DEFINITION EST16883 Aorta endothelial cells, TNF alpha-treated Homo sapiens

cDNA 5' end similar to amyloid, A4 beta subunit, mRNA sequence.

ACCESSION AA304003

VERSION AA304003.1 GI:1956491

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 354)

AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glocke, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, W.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 12140200
COMMENT On Jan 17, 1998 this sequence version replaced gi:1900069.
Other_ESTs: THC172078
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@etigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source
1. .354
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="ATCC (inhost):115766"
/db_xref="taxon:9606"
/clone.lib="Aorta endothelial cells, TNF alpha-treated"
/cell.type="endothelial cell"
/dev_stage="adult"
/note="Organ: aorta; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
BASE COUNT 102 a 80 c 92 g 78 t 2 others
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AA304003 ..
Align seg 1/1 to: AA304003 from: 1 to: 354

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
10 GATGCAGATTCGACATCGACTCAGATATGAGTTCATCATCAAAAA 57

seq_name: gb_est52:T49906

seq_documentation_block:
LOCUS T49906 383 bp mRNA EST 06-FEB-1995
DEFINITION Y99B06 r1 stratagene placenta (#937225) Homo sapiens cDNA clone
IMAGE:69779 5' similar to gb:X06989_rnal ALZHEIMER'S
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN), mRNA sequence.

ACCESSION T49906
VERSION T49906.1 GI:651766
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 383)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissole, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierri-Meg, J.,
Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 9704478
COMMENT On Nov 2, 1998 this sequence version replaced gi:3828645.
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
High quality sequence stop: 384.

FEATURES

source
1. .383
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:490676"
/db_xref="taxon:9606"
/clone.lib="IMAG:69779"
/clone.lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLAR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 113 a 81 c 103 g 86 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x T49906 ..
Align seg 1/1 to: T49906 from: 1 to: 383

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisHisGlnLys 16
|||||
61 GATGCAGATTCGACATCGACTCAGATATGAGTTCATCATCAAAAA 108

seq_name: gb_est51:R19709

seq_documentation_block:
LOCUS R19709 399 bp mRNA EST 17-APR-1995
DEFINITION Y935f04.r1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:34389 5' similar to gb:X06989_rnal ALZHEIMER'S DISEASE
AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION R19709
VERSION R19709.1 GI:774343
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On Jan 19, 1998 this sequence version replaced gi:2284625.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1369
High quality sequence stops: 214 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1369 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 214.

FEATURES

source

```
Location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="GB:406736"
/db_xref="taxon:9606"
/clone="IMAGE:34389"
/clone_lib="Soares infant brain L1NB"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/notes="organ: whole brain; Vector: L1mid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' RACTGGAGAATTCGCGCGCAGGAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the L1mid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
```

BASE COUNT

ORIGIN

104 a 85 c 106 g 94 t 10 others

alignment_scores:

Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x R19709 ..

Align seg 1/1 to: R19709 from: 1 to: 399

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||

219 GATGCGAATTCGACATGACTGAGTATGAGATTCATCATCAAAAA 266

seq_name: gb_est2:AA134479

seq_documentation_block:

LOCUS AA134479 417 bp mRNA EST 23-DEC-1997
DEFINITION ZO10904.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
cDNA clone IMAGE:567318 5' similar to gb:X06989_rnal ALZHEIMER'S
DISEASE AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Roefling, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Maria, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

TITLE

JOURNAL

MEDLINE

COMMENT

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1384 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 394.

FEATURES

source

```
Location/Qualifiers
1..417
/organism="Homo sapiens"
/db_xref="GB:459117"
/db_xref="taxon:9606"
/clone="IMAGE:567318"
/clone_lib="Stratagene neuroepithelium NT2RAMI 937234"
/dev_stage="Ntera-2/RA-MI neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2 (Ntera-2/ci.D1) precursor cells induced with Retinoic Acid for 1 week, followed by 3 weeks in mitotic inhibitors (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "
```

BASE COUNT

ORIGIN

110 a 93 c 117 g 95 t 2 others

alignment_scores:

Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-155-076-2 x AA134479 ..

Align seg 1/1 to: AA134479 from: 1 to: 417

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16

|||||

159 GATGCGAATTCGACATGACTGAGTATGAGATTCATCATCAAAAA 206

seq_name: gb_est16:AA124771

seq_documentation_block:

LOCUS AA124771 461 bp mRNA EST 11-SEP-1998
DEFINITION am61hl2.x1 Johnston frontal cortex Homo sapiens cDNA clone
IMAGE:1540103 3' similar to gb:X06989_rnal ALZHEIMER'S DISEASE
AMYLOID A4 PROTEIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krieman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, V., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilton RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

/clone_lib="BT0381"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 128 a 120 c 117 g 104 t
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent identity: 100.000
alignment_block:
US-09-155-076-2 x AW601576 ..
Align seg 1/1 to: AW601576 from: 1 to: 469

1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
422 GATGCAGAAATTCGACATCGACTCAGGATATGAAGTTCATCAAAAA 469

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 423.
Location/Qualifiers
1. .461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1540103"
/clone_lib="Johnston frontal cortex"
/sex="male"
/tissue_type="pooled frontal lobe"
/dev_stage="adult"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site_1:
EcoRI; Stanley NeuroPathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.
Random + oligo-dT primed into EcoRI site of ZAP II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
nlj@welchlink.welch.jhu.edu].
BASE COUNT 101 a 123 c 110 g 126 t 1 others
ORIGIN

alignment_scores:
Quality: 92.00 Length: 16
Ratio: 5.750 Gaps: 0
Percent Similarity: 100.000 Percent identity: 100.000

alignment_block:
US-09-155-076-2 x A1124771/rev ..
Align seg 1/1 to reverse of: A1124771 from: 1 to: 461
1 AspAlaGluPheArgHisAspSerGlyTyrGluValHisGlnLys 16
|||||
314 GATGCAGAAATTCGACATCGACTCAGGATATGAAGTTCATCAAAAA 267

seq_name: gb_est44:AW601576
seq_documentation_block:
LOCUS AW601576 469 bp mRNA EST 23-MAR-2000
DEFINITION QV3-BT0381-270100-073-f06 BT0381 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW601576
VERSION AW601576.1 GI:7306315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 469)
HGCP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT On Jan 6, 2000 this sequence version replaced gi:5677550.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV3st2-QV3-BT0381-270100-073-f06st3-2000-01-27st4-1>)
Seq primer: puc 18 forward
High quality sequence start: 111
High quality sequence stop: 469.
High quality sequence stop: 469.
location/Qualifiers
1. .469
/organism="Homo sapiens"
/db_xref="taxon:9606"

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 13, 2000, 02:25:00 ; Search time 17.65 seconds
(without alignments)
21.472 Million cell updates/sec

Title: US-09-155-076-2
Perfect score: 16
Sequence: 1 DAEFRHDSGYEVHQQ 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 188963 seqs, 23686106 residues
Word size : 0

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	16	100.0	16	1 R60371	Beta-amyloid (1-16)
2	16	100.0	16	1 W35344	Human beta-amyloid
3	16	100.0	21	1 W08361	Beta-secretase sub
4	16	100.0	22	1 R07753	Beta-amyloid protri
5	16	100.0	28	1 P90381	Synthetic A4 amylo
6	16	100.0	28	1 R54702	Beta-amyloid fragm
7	16	100.0	28	1 R60368	Beta-amyloid (1-28
8	16	100.0	28	1 W01413	Beta/A4-amyloid pe
9	16	100.0	28	1 W01414	Beta/A4-amyloid pe
10	16	100.0	28	1 R64170	A4-O(1-28), a parti
11	16	100.0	28	1 R64172	A4-B(1-28), a parti
12	16	100.0	28	1 W81467	Synthetic amyloid
13	16	100.0	30	1 W81468	Synthetic amyloid
14	16	100.0	33	1 W08359	Beta-secretase sub
15	16	100.0	33	1 W81469	Synthetic amyloid
16	16	100.0	33	1 W98002	Amyloid precursor
17	16	100.0	35	1 W02335	Beta-amyloid pepti
18	16	100.0	35	1 W47228	Beta-amyloid pepti
19	16	100.0	35	1 W89355	Beta-amyloid pepti
20	16	100.0	35	1 W89359	Beta-amyloid pepti
21	16	100.0	36	1 W81471	Synthetic amyloid
22	16	100.0	38	1 R60362	Beta-amyloid (1-38
23	16	100.0	38	1 W92722	Human tachykinin a
24	16	100.0	39	1 R60363	Beta-amyloid (1-39
25	16	100.0	39	1 W81472	Synthetic amyloid
26	16	100.0	40	1 R33191	Beta-amyloid pepti
27	16	100.0	40	1 R60364	Beta-amyloid (1-40
28	16	100.0	40	1 W23335	Amyloid beta pepti
29	16	100.0	40	1 W37507	Amyloid beta prote
30	16	100.0	40	1 W47232	Beta-amyloid pepti
31	16	100.0	40	1 W47226	Beta-amyloid pepti
32	16	100.0	40	1 W81473	Synthetic amyloid
33	16	100.0	40	1 W92723	Human tachykinin a

ALIGNMENTS

RESULT 1

R60371
ID R60371 standard; peptide; 16 AA.
AC R60371, 1995 (first entry)
DT 15-MAR-1995
DE Beta-amyloid (1-16).
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
OS Homo sapiens.
PN W09417197-A.
PD 04-AUG-1994.
PF 24-JAN-1994; J00089.
PR 25-JAN-1993; JP-010132.
PR 05-FEB-1993; JP-019035.
PR 16-NOV-1993; JP-286985.
PR 28-DEC-1993; JP-334773.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Kitada C, Odaoka A, Suzuki N;
DR WPI; 94-264110/32.
PT Antibodies recognising specific parts of beta-amyloid - can be used for diagnosis of diseases implicating beta-amyloid, such as Alzheimer's disease
PT Alzheimer's disease
PS Claim 7; Page 85; 116pp; Japanese.
CC Antibodies which recognise specific subfragments of the beta-amyloid protein are claimed. Specifically, the antibodies (which are pref. monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal portion of beta-amyloid or they recognise residues 25-35 or 35-43 from the C-terminal portion. The antibodies are useful for assaying beta-amyloid and its derivatives for diagnosis of Alzheimer's disease.
CC Sequence 16 AA;

Query Match 100.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.6e-12; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0;

QY 1 DAEFRHDSGYEVHQQ 16

Db 1 DAEFRHDSGYEVHQQ 16
|||||

RESULT 2

W35344
ID W35344 standard; peptide; 16 AA.
AC W35344;
DT 17-APR-1998 (first entry)
DE Human beta-amyloid precursor 16-mer peptide.
KW Beta-amyloid precursor polypeptide; acetylcholinesterase; AChE;
neuronal degeneration; Parkinson's disease; Alzheimer's disease;
stroke; cancer; calcium channel modulator; antibody; inhibitor.
OS Homo sapiens.
PN W09735962-A1.
PD 02-OCT-1997.
PF 21-MAR-1997; G00796.
PR 22-MAR-1996; GB-006040.

Wild type aggregat
Alzheimer's amyloi
Beta-amyloid (1-41
Beta-amyloid pepti
Sequence of A99 (b
Beta-amyloid pepti
Beta-amyloid (1-42
Beta amyloid pepti
Beta amyloid pepti
Beta amyloid pepti
Beta amyloid pepti
Alzheimer amyloid

34 16 100.0 40 1 W99584
35 16 100.0 41 1 R22206
36 16 100.0 41 1 R60365
37 16 100.0 41 1 R65283
38 16 100.0 42 1 R20330
39 16 100.0 42 1 R33192
40 16 100.0 42 1 R60366
41 16 100.0 42 1 R65285
42 16 100.0 42 1 R65286
43 16 100.0 42 1 R65287
44 16 100.0 42 1 R65288
45 16 100.0 42 1 R94591

PA (ISIS-) ISIS INNOVATION LTD.
 PI Greenfield SA, Vaux DJ;
 DR WPI: 97-489626/45.
 PT Peptide(s) from acetylcholine esterase which open calcium channels -
 PT used for treating disorders of the central nervous system, cancer
 PT and stroke
 PS Claim 3; Page 20; 27pp; English.
 CC This 16-mer peptide is present in a region of the beta-amyloid precursor
 CC polypeptide. This region lies at the amino acid terminus of the 42
 CC residue peptide which accumulates in Alzheimer's disease. The 16-mer
 CC has at least 70% homology with the beta-amyloid precursor. This peptide
 CC is known to act alone or in synergism with a fragment of
 CC acetylcholinesterase (W5340-W5343) to contribute to neuronal
 CC degeneration. Compounds that inhibit the biological activity of the
 CC novel peptides, and antibodies, can be used to control cytoplasmic
 CC calcium ion currents in vivo, and are useful for treating disorders of
 CC the central nervous system (e.g. Parkinson's and Alzheimer's diseases),
 CC stroke and cancer.
 SQ Sequence 16 AA;

Query Match 100.0%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.6e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 DB 1 DAEFRHDSGYEVHHQK 16

RESULT 3

ID W08361 standard; peptide; 21 AA.
 AC W08361;
 DT 05-SEP-1997 (first entry)
 DE Beta-secretase substrate #3.
 KW Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase;
 KW alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.
 OS Synthetic.
 PN W09640885-A2.
 PD 19-DEC-1996.
 PF 07-JUN-1996; U09985.
 PR 07-JUN-1995; US-487152.
 PR 07-JUN-1995; US-480498.
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
 PI McConlogue LC, Sinha S, Tan H;
 DR WPI: 97-052304/05.
 PT Beta-secretase which specifically cleaves beta-amyloid precursor
 PT protein - useful to screen for inhibitors useful in treatment of
 PT Alzheimer's disease
 PS Disclosure; Page 45; 92pp; English.
 CC W08359-W08362 represent substrates for the enzyme of the invention. The
 CC enzyme of the invention is beta-secretase, and specifically cleaves
 CC beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP
 CC is thought to occur via cleavage between residues 16 and 17 of the
 CC beta-amyloid peptide region by an alpha-secretase. Pathogenic processing
 CC is thought to occur by beta-secretase cleavage of beta-APP.
 CC Beta-secretase activity can be detected and measured using a method of
 CC the invention, which detects at least one of the beta-secretase cleavage
 CC products formed on cleavage. The method can be used to determine whether
 CC a test substance inhibits proteolytic cleavage, by beta-secretase, of
 CC beta-APP. Compounds effective to at least partially inhibit
 CC beta-secretase activity can be used to inhibit cleavage of beta-APP in
 CC cells or mammalian hosts. Isolation and purification of beta-secretase
 CC will permit chemical modelling of a critical event in the pathology of
 CC Alzheimer's disease.
 SQ Sequence 21 AA;

Query Match 100.0%; Score 16; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 7.1e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 DB 6 DAEFRHDSGYEVHHQK 21

RESULT 4

ID R07753 standard; protein; 22 AA.
 AC R07753;
 DT 22-FEB-1991 (first entry)
 DE Bta-amyloid protein, SCVAP2.
 KW Monoclonal antibody SV17-6E10; Down's syndrome; Alzheimer's disease;
 KW beta-amyloid precursor; amyloid plaques.
 OS Synthetic.
 PN W09012871-A.
 PD 01-NOV-1990.
 PF 13-APR-1990; US-338983.
 PR 14-APR-1989; US-338983.
 PA (REME-) RES FOUND MENTAL HY.
 PI Kim KS, Wisniewski HM, Wen GY, Chen CMJ, Sapienza VJ;
 DR WPI: 90-348474/46.
 PT Cerebrovascular amyloid protein-specific monoclonal antibody
 PT SV17-6E10 - for immunosay of peptide whose levels are raised in
 PT Down's syndrome or Alzheimer's disease patients
 PS Example 4; page 11; 24pp; English.
 CC This peptide is used in a "Double Ab Sandwich Immunoassay" to
 CC detect beta-amyloid protein. SV17-6E10 MAb(capture Ab) is used
 CC to coat microtitre plate wells. The plate is then washed (dist-
 CC illed water), coated with PBS(IGB) and this (SCVAP2) protein is
 CC added. The plate is washed and a 2nd Ab (detection Ab), MAb 4G8-
 CC This double Ab sandwich ELISA test is a highly sensitive and
 CC accurate detection system for the beta-amyloid protein.
 CC See also R07752.
 SQ Sequence 22 AA;

Query Match 100.0%; Score 16; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 7.4e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
 |||||
 DB 1 DAEFRHDSGYEVHHQK 16

RESULT 5

ID P90381 standard; protein; 28 AA.
 AC P90381;
 DT 1-NOV-1989 (first entry)
 DE Synthetic A4 amyloid peptide
 KW Synthetic; A4 amyloid polypeptide; Alzheimer's disease;
 KW immunoassays; antibodies.
 OS Synthetic
 PN W08906242-A.
 PD 13-JUL-1989.
 PF 11-OCT-1988; U03590.
 PR 08-OCT-1987; US-105751.
 PA (MCLE) McLean Hospital Corp; (UYRO) University of Rochester.
 PI Majocha R, Marotta CA, Zain S;
 DR WPI: 89-220551/30.
 PT Antibodies to A4 amyloid polypeptide
 PT - used in immunoassays and for imaging of A4 amyloid
 PT in Alzheimer's diseased patients.
 PS Claim 1; page 27; 30pp; English.
 CC Synthetic A4 amyloid polypeptide (see also P90382, P90383).
 CC Used as immunogen, (un)coupled, or to produce antibodies. used in
 CC immunoassays and for imaging of A4 amyloid in Alzheimer's disease.
 SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 6
R54702
ID R54702 standard; peptide; 28 AA.
AC R54702;
DT 15-DEC-1994 (first entry)
DE Beta-amyloid fragment (1-28).
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
OS Homo sapiens.
PN W09409364-A.
FD 28-APR-1994.
FF 13-OCT-1993; U09772.
PR 13-OCT-1992; US-959251.
PA (UYDU-) UNIV DUKE.
PI Strittmatter WJ.
DR WPI; 94-151484/18.
PT Immobilised beta-amyloid protein or fragments - used in assays
for obtaining prods for use in the diagnosis and treatment of
PT disorders such as Alzheimer's disease.
PS Claim 4; Page 28; 49pp; English.
CC A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
the peptides given in R54702-03) immobilised on a solid support can be
used to detect cpds. which bind to BAP. Binding of proteins in
CC human cerebrospinal fluid proteins were shown to bind to beta-
CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)
CC was used as control.
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 7
R60368
ID R60368 standard; peptide; 28 AA.
AC R60368;
DT 15-MAR-1995 (first entry)
DE Beta-amyloid (1-28).
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
OS Homo sapiens.
PN W09417197-A.
PD 04-AUG-1994.
PF 24-JAN-1994; J00089.
PR 25-JAN-1993; JP-010132.
PR 05-FEB-1993; JP-019035.
PR 16-NOV-1993; JP-286985.
PR 28-DEC-1993; JP-334773.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Kitada C, Odaka A, Suzuki N;
DR WPI; 94-264110/32.
PT Antibodies recognising specific parts of beta-amyloid - can be
used for diagnosis of diseases implicating beta-amyloid, such as,
PT Alzheimer's disease.
PS Claim 7; Page 84; 116pp; Japanese.
CC Antibodies which recognise specific subfragments of the beta-amyloid
CC protein are claimed. Specifically, the antibodies (which are pref.
CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
CC from the C-terminal portion. The antibodies are useful for assaying

CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
CC disease.
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 8
W01413
ID W01413 standard; Protein; 28 AA.
AC W01413;
DT 20-JAN-1997 (first entry)
DE Beta/A4-amyloid peptide; tissue plasminogen activator;
KW Beta/A4-amyloid peptide; investigation; pathogenesis;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
KW hemorrhage.
OS Homo sapiens.
PN W09615799-A1.
PD 30-MAY-1996.
PF 22-NOV-1995; U15007.
PR 22-NOV-1994; US-347144.
PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
PI Anderson S;
DR WPI; 96-288332/27.
PT Use of agents which bind beta-amyloid peptide - for diagnosis,
PT prevention and treatment of vascular damage caused by amyloid
PT deposits, Part 1; Fig 1; 52pp; English.
PS Example 1; Fig 1; 52pp; English.
CC To investigate the effects of beta-amyloid peptide (BAP) on
CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
CC One peptide contained 42 amino acids and corresp. to the full
CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained
CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
CC (HCHWA-D), respectively. In an assay to determine the effect of
CC the peptides on t-PA activation, each peptide (R95248, 49 and 50)
CC gave 1st order rate constant of activation (k_{app}) values of
CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
CC and fibrinogen controls. The results demonstrate that the BAP are
CC able to stimulate t-PA activity in vitro, which is significant in
CC that it provides a means for investigating and controlling the
CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
CC angiopathy related cerebral haemorrhage.
SQ Sequence 28 AA;

Query Match 100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

RESULT 9
W01414
ID W01414 standard; Protein; 28 AA.
AC W01414;
DT 20-JAN-1997 (first entry)
DE Beta/A4-amyloid peptide residues 1-28 Dutch.
KW Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
KW Alzheimer's disease; stimulation; investigation; pathogenesis;
KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;

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control; cerebral amyloid angiopathy; cerebral; haemorrhage;
 KW hemorrhage.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 22 /note= "wild type Glu substd. with Gln"
 FT
 PN WO9615799-A1.
 PD 30-MAY-1996.
 PF 22-NOV-1995; U15007.
 PR 22-NOV-1994; US-347144.
 PA (RUTG) UNIV RUTGERS STATE NEW JERSEY.
 PI Anderson S;
 PT WPI; 96-268332/27.
 PR Use of agents which bind beta-amyloid peptide - for diagnosis,
 PT prevention and treatment of vascular damage caused by amyloid
 PT deposits, partic. in haemorrhaging and Alzheimer's disease
 PS Example 1; Fig 1; 52pp; English.
 CC To investigate the effects of beta-amyloid peptide (BAP) on
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
 CC One peptide contained 42 amino acids and corresp. to the full
 CC length BAP (R95248). The other 2 peptides (R95249 and 50) contained
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
 CC (HCHWA-D), respectively. In an assay to determine the effect of
 CC the peptides on t-PA activation, each peptide (R95248, 49 and 50)
 CC gave 1st order rate constant of activation (k(app)) values of
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
 CC and fibrinogen controls. The results demonstrate that the BAP are
 CC able to stimulate t-PA activity in vitro, which is significant in
 CC that it provides a means for investigating and controlling the
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
 CC angiopathy related cerebral haemorrhage.
 CC Sequence 28 AA;
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 16; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 10
 R64170
 ID R64170 standard; peptide; 28 AA.
 AC R64170;
 DT 03-AUG-1995 (first entry)
 DE A4-O(1-28) a partial beta amyloid peptide.
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
 KW Down's syndrome; A4-O(1-28).
 OS Synthetic.
 PN WO9428412-A.
 PD 08-DEC-1994.
 PF 27-MAY-1994; U05809.
 PR 28-MAY-1993; US-069010.
 PA (MIRI-) MIRIAM HOSPITAL.
 PI Majocha RE, Marotta CA;
 PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier - useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 PS Example 3; Page 23; 58pp; English.
 CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the
 CC 28 amino acids are different from the A4-O(1-28) peptide shown in R64170.
 CC A4-O has strong aggregation properties, and binds to itself strongly. It
 CC is used to obtain and select beta amyloid proteins that can be used for
 CC in vivo imaging of amyloid deposits and hence diagnosis of an
 CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165
 CC shows the generic sequence of the amyloid protein for generation of
 CC variants.
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 16; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 11
 R64172
 ID R64172 standard; peptide; 28 AA.
 AC R64172;
 DT 03-AUG-1995 (first entry)
 DE A4-B(1-28) a partial beta amyloid peptide.
 KW beta amyloid protein; mutant; variant; detection; amyloid deposition;
 KW diagnosis; amyloidosis associated disease; Alzheimer's disease;
 KW Down's syndrome; A4-B(1-28).
 OS Synthetic.
 PN WO9428412-A.
 PD 08-DEC-1994.
 PF 27-MAY-1994; U05809.
 PR 28-MAY-1993; US-069010.
 PA (MIRI-) MIRIAM HOSPITAL.
 PI Majocha RE, Marotta CA;
 PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier - useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 PS Example 3; Page 23; 58pp; English.
 CC AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of the
 CC 28 amino acids are different from the A4-O(1-28) peptide shown in R64170.
 CC A4-O has strong aggregation properties, and binds to itself strongly. It
 CC is used to obtain and select beta amyloid proteins that can be used for
 CC in vivo imaging of amyloid deposits and hence diagnosis of an
 CC amyloidosis-associated disease, such as AD or Down's syndrome. R64165
 CC shows the generic sequence of the amyloid protein for generation of
 CC variants.
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 16; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEFRHDSGYEVHHQK 16
 DB 1 DAEFRHDSGYEVHHQK 16
 RESULT 12
 W81467
 ID W81467 standard; peptide; 28 AA.
 AC W81467;
 DT 28-JAN-1999 (first entry)
 DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.
 OS Synthetic.
 PN US5840838-A.
 PD 24-NOV-1998.
 PF 29-FEB-1996; 609090.
 PR 29-FEB-1996; US-609090.
 PA (KENT) UNIV KENTUCKY RES FOUND.
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
 DR WPI; 99-034120/03.
 PT Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity
 PT Claim 5; Columns 9-10; 14pp; English.
 PS

Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Query Match 100.0%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.2e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 13

W81468 ID W81468 standard; peptide; 30 AA.

AC W81468

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).

KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 609090.

PR 29-FEB-1996; US-609090.

PA (KENT) UNIV KENTUCKY RES FOUND.

PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
WPI: 99-034120/03.

DR Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PT Claim 5; Columns 9-10; 14pp; English.

PS Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical generating capacity and glutamine synthetase inactivation.

Sequence 30 AA;

Query Match 100.0%; Score 16; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||

Db 1 DAEFRHDSGYEVHHQK 16

RESULT 14

W81468 ID W81468 standard; peptide; 30 AA.

AC W81468

DT 05-SEP-1997 (first entry)

DE Beta-secretase substrate #1.

Beta-cleavage site; beta amyloid precursor protein; APP; beta-secretase; alpha-secretase; proteolytic cleavage; inhibitor; Alzheimer's disease.

OS Synthetic.

PN WO9640885-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; U09985.

PR 07-JUN-1995; US-485152.

PR 07-JUN-1995; US-480498.

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PI Anderson JP, Chrysler SMS, Jacobson-croak KL, Keim PS;
McDonlogue LC, Sinha S, Tan H;
WPI: 97-052304/05.

DR Beta-secretase which specifically cleaves beta-amyloid precursor protein - useful to screen for inhibitors useful in treatment of Alzheimer's disease

PT Disclosure; Page 44; 92pp; English.

PS WO8359-W08362 represent substrates for the enzyme of the invention. The enzyme of the invention is beta-secretase, and specifically cleaves beta-amyloid precursor protein (beta-APP). Normal processing of beta-APP is thought to occur via cleavage between residues 16 and 17 of the beta-amyloid peptide region by an alpha-secretase. Pathogenic processing is thought to occur by beta-secretase cleavage of beta-APP.

CC Beta-secretase activity can be detected and measured using a method of the invention, which detects at least one of the beta-secretase cleavage products formed on cleavage. The method can be used to determine whether a test substance inhibits proteolytic cleavage, by beta-secretase, of beta-APP. Compounds effective to at least partially inhibit beta-secretase activity can be used to inhibit cleavage of beta-APP in cells or mammalian hosts. Isolation and purification of beta-secretase will permit chemical modelling of a critical event in the pathology of Alzheimer's disease.

CC Sequence 33 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQK 16
|||||

Db 18 DAEFRHDSGYEVHHQK 33

RESULT 15

W81469 ID W81469 standard; peptide; 33 AA.

AC W81469

DT 28-JAN-1999 (first entry)

DE Synthetic amyloid beta (Abeta) peptide 4 (residues 1-33).

KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
research; neurotoxicity; free-radical; glutamine synthetase.

OS Synthetic.

PN US5840838-A.

PD 24-NOV-1998.

PF 29-FEB-1996; 609090.

PR 29-FEB-1996; US-609090.

PA (KENT) UNIV KENTUCKY RES FOUND.

PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
WPI: 99-034120/03.

DR Process for treating synthetic amyloid beta peptides - by organic solvent treatment, useful for studying neurotoxicity

PT Claim 5; Columns 9-10; 14pp; English.

PS Sequences W81466 to W81476 represent synthetic amyloid beta (Abeta) peptides. The invention provides a process for treating a synthetic Abeta peptide that comprises dissolving the peptide in a deoxygenated solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and acetonitrile to a concentration of 0.01-10 mg/ml, incubating the solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta peptides are useful as research tools for studying neurotoxicity resulting from Abeta peptide enhanced free-radical production. The treatment increases the activity of the synthetic Abeta peptides in tests to determine free-radical

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CC generating capacity and glutamine synthetase inactivation.
SQ Sequence 33 AA;

Query Match 100.0%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAEFRHDSGYEVHHQK 16
| | | | | | | | | | | | | | | | | | | | | |
Db 1 DAEFRHDSGYEVHHQK 16

Search completed: September 13, 2000, 02:25:00
Job time: 173 sec